

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 11, 2004, 00:41:05 ; Search time 9096.67 Seconds
(without alignments)
12582.818 Million cell updates/sec

Title: US-09-830-972-28
Perfect score: 3833
Sequence: 1 ctatctcctctctcagccgc.....ttaaaaaaaaaaaaaaaaaaaaa 3833

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*

28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			Query				Description
	No.	Score	Match	Length	DB	ID	
	1	986	25.7	1798	11	AF125103	AF125103 Homo sapi
	2	915.6	23.9	1785	11	AF077050	AF077050 Homo sapi
	3	774.2	20.2	3533	11	AK034902	AK034902 Mus muscu
c	4	668.6	17.4	956	9	AL573494	AL573494 AL573494
	5	646.8	16.9	896	14	CB204418	CB204418 AGENCOURT
	6	642	16.7	1003	14	CK231727	CK231727 ILLUMIGEN
	7	634.2	16.5	1101	14	CF110956	CF110956 Shultzomi
	8	631	16.5	871	13	BQ719894	BQ719894 AGENCOURT
	9	628.8	16.4	646	14	CB467517	CB467517 733269 MA
	10	625.4	16.3	627	12	BM986175	BM986175 LM24HW001
	11	621.4	16.2	843	12	BG570231	BG570231 602590632
	12	619	16.1	619	14	CF768055	CF768055 CES004952
	13	618.6	16.1	1164	14	CK232009	CK232009 ILLUMIGEN
	14	617	16.1	631	10	BF044381	BF044381 BP250021B
	15	614.2	16.0	822	14	CB521332	CB521332 UI-M-GH0-
	16	605.2	15.8	901	13	BQ879359	BQ879359 AGENCOURT
	17	591.4	15.4	593	10	BF039928	BF039928 BP250015A
c	18	588.8	15.4	606	14	CF765999	CF765999 CES000103
	19	587	15.3	587	12	BI775114	BI775114 467491 MA
	20	581.2	15.2	958	12	BM801698	BM801698 AGENCOURT
c	21	580	15.1	996	10	BF570468	BF570468 602186269
	22	572.6	14.9	969	12	BG706140	BG706140 602669409
c	23	568.8	14.8	598	14	CB534701	CB534701 768054 MA
	24	568.8	14.8	730	12	BI601346	BI601346 603245090
	25	567.6	14.8	986	13	BU841009	BU841009 AGENCOURT
	26	566	14.8	882	13	BQ233389	BQ233389 AGENCOURT
	27	565	14.7	579	14	CB222263	CB222263 11L25H09
	28	564.8	14.7	819	12	BG109465	BG109465 602280543
	29	564	14.7	772	14	CF948588	CF948588 UI-M-HJ0-
	30	564	14.7	842	13	BU709149	BU709149 UI-M-EW0-
	31	562	14.7	1022	12	BM557554	BM557554 AGENCOURT
c	32	560.8	14.6	783	12	BQ001312	BQ001312 UI-H-DH1-
	33	558.8	14.6	598	14	CF118424	CF118424 fs543.z1
c	34	558	14.6	789	13	BU619407	BU619407 UI-H-FL1-
c	35	557.8	14.6	586	14	CB534657	CB534657 768008 MA
	36	557.4	14.5	578	14	CF762449	CF762449 CES000069
	37	557.2	14.5	845	9	AL533461	AL533461 AL533461
	38	556.8	14.5	707	14	CF793493	CF793493 888888 MA
	39	556.8	14.5	954	12	BM470283	BM470283 AGENCOURT
c	40	556.4	14.5	741	14	CB169095	CB169095 IMU602702
	41	556.2	14.5	650	14	CB215381	CB215381 NISC_np05
	42	556	14.5	556	10	BF039736	BF039736 BP250014B
	43	553	14.4	699	12	BG819566	BG819566 602783209
	44	552.6	14.4	758	12	BG697436	BG697436 602660623
	45	552	14.4	785	14	CA511870	CA511870 UI-R-FJ0-

ALIGNMENTS

RESULT 1

AF125103

LOCUS AF125103 1798 bp mRNA linear HTC 22-MAY-2001

DEFINITION Homo sapiens neuroendocrine specific protein c homolog mRNA,
complete cds.

ACCESSION AF125103

VERSION AF125103.1 GI:5107001

KEYWORDS HTC.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1798)

AUTHORS Zhang,Q.H., Ye,M., Wu,X.Y., Ren,S.X., Zhao,M., Zhao,C.J., Fu,G.,
Shen,Y., Fan,H.Y., Lu,G., Zhong,M., Xu,X.R., Han,Z.G., Zhang,J.W.,
Tao,J., Huang,Q.H., Zhou,J., Hu,G.X., Gu,J., Chen,S.J. and Chen,Z.TITLE Cloning and functional analysis of cDNAs with open reading frames
for 300 previously undefined genes expressed in CD34+ hematopoietic
stem/progenitor cells

JOURNAL Genome Res. 10 (10), 1546-1560 (2000)

MEDLINE 20499367

PUBMED 11042152

REFERENCE 2 (bases 1 to 1798)

AUTHORS Ye,M., Zhang,Q., Zhou,J., Shen,Y., Guan,Z., Wu,X., Fan,H., Mao,H.,
Dai,M., Huang,Q., Chen,S. and Chen,Z.

TITLE Human neuroendocrine specific protein c homolog mRNA, complete cds

JOURNAL Unpublished

REFERENCE 3 (bases 1 to 1798)

AUTHORS Ye,M., Zhang,Q., Zhou,J., Shen,Y., Guan,Z., Wu,X., Fan,H., Mao,H.,
Dai,M., Huang,Q., Chen,S. and Chen,Z.

TITLE Direct Submission

JOURNAL Submitted (02-FEB-1999) Shanghai Institute of Hematology, Shanghai
Second Medical University, Rui-Jin Hospital, 197 Rui-Jin Road II,
Shanghai 200025, P. R. China

FEATURES Location/Qualifiers

source

1. .1798

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/cell_type="CD34+ hematopoietic stem/progenitor cells"

CDS

215. .814

/codon_start=1

/product="neuroendocrine specific protein c homolog"

/protein_id="AAD39920.1"

/db_xref="GI:5107002"

/translation="MDGQKKNWKDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIV
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YLERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE"

ORIGIN

Query Match

25.7%; Score 986; DB 11; Length 1798;

Db 1021 GCTATGTATGGATTTAAACCGTAATCATATCTTTTTCTATCTATCTGAGGCACTGGTGG 1080

Qy 3129 ATAAACAAAGATCTGAGAAAGCTGTATATTACACTTTGTGCGCAGGTAGTCTTGCTGTAT- 3187
| | | | | | | | | | | | | | | | | | | | | | | |

Db 1081 AATAAAAAAC-----CTGTATATTTTACTTTGTTGCAGATAGTCTTGCCGCATC 1129

Qy 3188 TTGGGGAATTGCAAAGAAAGTGGAGCT-----GACAGAAATAACCCTTTTTCAGTTTG 3241
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Db 1130 TTGGCAAGTTGCAGAGATGGTGGAGCTAGAAAAAAAAAAAAAAAAAGCCCTTTTCAGTTTG 1189

Qy 3242 TGCACTGTGTACGGTCTGTGTAGGTTGATGCAGATTTTCTGAAATGAAA---TGTTTAG 3297
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Db 1190 TGCACTGTGTATGGTCCGTGTAGATTGATGCAGATTTTCTGAAATGAAATGTTTGTAG 1249

Qy 3298 ACGAGATCATGCCACCAAGGCAGGAGTGAAAAAGCTTGCCTTTCTGGTATGTTCTAGGT 3357
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Db 1250 ACGAGATCATACCGGTAAAGCAGGAATGACAAAGCTTG-CTTTTCTGGTATGTTCTAGGT 1308

Qy 3358 GTATTGTGAAATTTACTGTTGTATTAATTGCCAATATAAGTAAATATAGATTATATATAT 3417
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Db 1309 GTATTGTGACTTTTACTGTTATATTAATTGCCAATATAAGTAAATATAGATTATA----- 1363

Qy 3418 CTATATATAGTGTTTCACGAAGCTTAGCCCTTTACCTTCCCAGCTGCCCCACAGTGCTTG 3477
| | | | | | | | | | | | | | | | | | | | | | | |

Db 1364 -TATGTATAGTGTTTCACAAAGCTTAGACCTTTACCTT-CCAGCCACCCACAGTGCTTG 1421

Qy 3478 ATACT-----TCTGTCATGGGTTTTATGTGTGTAGTCCCAAAGCACATAAGCTAGGGAG 3531
| | | | | | | | | | | | | | | | | | | | | | | |

Db 1422 ATATTTTCAGAGTCAGTCATTGGTTATACATGTGTAGTTCCCAAAGCACATAAGCTAGAAGA 1481

Qy 3532 AAACGTACTTCTAGGCGCACTACCATCTGTTTTCAACACGAACCGACGCCATGCAAACAG 3591
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Db 1482 AGAAATATTTCTAGGAGCACTACCATC-GTTTTCAACATGAA---ATGCCACACACATAG 1537

Qy 3592 AACTCC-TCAACATAAACTTCACTGCACAGACTTACTGTAGTTAATTTTATCACA--AAC 3648
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Db 1538 AACTCCAACAACATCAATTTCACTGCACAGACTGACTGTAGTTAATTTTGTACAGGATC 1597

Qy 3649 TCTGGACTGAATCTAATGCTTCCAAAAA-----TGTTTGCAAATATCAAACATTGTTA 3701
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Db 1598 TATGGACTGAATCTAATGCTTCCAAAAATGTTGTTTGTGTTTGCAAATATCAAACATTGTTA 1657

Qy 3702 TGTAAGAAAATAT-----AAATGACGATTTATACAATTGTGGTTTAAGCTGTATTGA 3753
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Db 1658 TGCAAGAAATTATTAATTACAAAATGAAGATTTATACCATTGTGGTTTAAGCTGTACTGA 1717

Qy 3754 ACTAAATCTGTGGAATGCATTGTGAACTGTAAAAGCAAAGTATCAATAAAGCTTATAGAC 3813
| | | | | | | | | | | | | | | | | | | | | | | |

Db 1718 ACTAAATCTGTGGAAGGCATTGTAACTGTAAAAGCAAAGTATCAATAAAGCTTATAGAC 1777

Qy 3814 TTAAAAAAAAAAAAAAAAAAAA 3833
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Db 1778 CCAAAACGAAAAAAAAAAAAA 1797

LOCUS AF077050 1785 bp mRNA linear HTC 21-NOV-2002
 DEFINITION Homo sapiens neuroendocrine-specific protein C homolog mRNA, complete cds.
 ACCESSION AF077050
 VERSION AF077050.1 GI:4689147
 KEYWORDS HTC.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1785)
 AUTHORS Song,H., Peng,Y., Zhou,J., Huang,Q., Dai,M., Mao,Y., Yu,Y., Xu,X., Luo,B., Hu,R. and Chen,J.
 TITLE Human neuroendocrine-specific protein C (NSP) homolog gene
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 1785)
 AUTHORS Song,H.
 TITLE Direct Submission
 JOURNAL Submitted (10-JUL-1998) Rui-Jin Hospital, Shanghai Institute of Endocrinology, Molecular Medical Center, 197 Rui-Jin Road II, Shanghai 200025, P.R. China
 FEATURES
 source Location/Qualifiers
 1. .1785
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /tissue_type="pituitary"
 CDS
 214. .813
 /codon_start=1
 /product="neuroendocrine-specific protein C homolog"
 /protein_id="AAD27783.1"
 /db_xref="GI:4689148"
 /translation="MDGQKKNWKDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGFALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE"

ORIGIN

Query Match 23.9%; Score 915.6; DB 11; Length 1785;
 Best Local Similarity 85.5%; Pred. No. 1.5e-156;
 Matches 1238; Conservative 0; Mismatches 144; Indels 66; Gaps 17;

QY 2304 GTTGTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGC 2363
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 Db 247 GTTGTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGC 306
 QY 2364 TTGTTCTGCTGCTCTCGCTGACAGTATTCAGCATTGTGAGTGTAACGGCCTACATTGCC 2423
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 Db 307 CTATTCCTGCTGCTTTCATTGACAGTATTCAGCATTGTGAGCGTAACAGCCTACATTGCC 366
 QY 2424 TTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAAGGGTGTGATCCAGGCTATC 2483
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 Db 367 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC 426
 QY 2484 CAGAAATCTGATGAAGGCCACCCATTAGGGCATATTTGGAATCTGAAGTTGCTATATCT 2543
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 Db 427 CAGAAATCAGATGAAGGCCACCCATTAGGGCATATCTGGAATCTGAAGTTGCTATATCT 486

Qy	2544	GAGGAGTTGGTTCAGAAGTACAGCAATTCTGCTCTTGGTCATGTTAAGTGCACAATAAAA	2603
Db	487	GAGGAGTTGGTTCAGAAGTACAGTAATTCTGCTCTTGGTCATGTGAAGTGCACGATAAAG	546
Qy	2604	GAAGTCAGACGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTG	2663
Db	547	GAAGTCAGGCGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTG	606
Qy	2664	ATGTGGGTATTTACCTATGTTGGTGCCTTGTTCAATGGTCTGACACTACTAATTTTGGCT	2723
Db	607	ATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAATGGTCTGACACTACTGATTTTGGCT	666
Qy	2724	CTGATTTCACTCTTCAGTGTTCTGTTATTTATGAACGGCATCAGGCGCAAATAGATCAT	2783
Db	667	CTCATTTCACCTCTTCAGTGTTCTGTTATTTATGAACGGCATCAGGCACAGATAGATCAT	726
Qy	2784	TATCTGGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATC	2843
Db	727	TATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATC	786
Qy	2844	CCTGGATTGAAGCGTAAAGCTGAATGAGAAAGCCTGAAAGAGTTAACAATAGAGGAGTTT	2903
Db	787	CCTGGATTGAAGCGCAAAGCTGAATGAAAACGCCCAAATAATTA-----GTAGGAGTTC	841
Qy	2904	ATCTTTAAAGGGGATATTCATTTGATTCCATTGGGGAGGGTCAGGGAAGAACAAGCCTT	2963
Db	842	ATCTTTAAAGGGGATATTCATTTGATTATACGGGGAGGGTCAGGGAAGAACGAA-CCTT	900
Qy	2964	GACATTGCAGTGCAGTTTCAC-----AGATCTTTATTTTGTAGCAACGCAGTGTC	3012
Db	901	GACGTTGCAGTGCAGTTTCACAGATCGTTGTTAGATCTTTATTTTGTAGCCATGCAGTGTT	960
Qy	3013	-TGAGGAAAAATGACCTGTCTTGACTGCCCTGTGTTTCATCATCTTAAGTATTGTAAGCTG	3071
Db	961	GTGAGGAAAAATTACCTGTCTTGACTGCCATGTGTTTCATCATCTTAAGTATTGTAAGCTG	1020
Qy	3072	CTATGTATGGATTAAATCGTAATCATATTTGTTTTCTGTATGAGGCACTGGTGAATA	3131
Db	1021	CTATGTATGGATTAAACCGTAATCATA--TCTTTTCTATCTGAGGCACTGGTGA--	1076
Qy	3132	AACAAAGATCTGAGAAAGCTGTATATTACACTTTGTCGCAGGTAGTCTTGCTGTAT-TTG	3190
Db	1077	-----ATAAAAAACCTGTATATTTTACTTTGTTGCAGATAGTCTTGCCGCATCTTG	1127
Qy	3191	GGGAATTGCAAAGAAAGTGGAGCT-----GACAGAAATAACCCTTTTACAGTTTGTG	3243
Db	1128	GCAAGTTGCAGAGATGGTGGAGCTAGAAAAAAAAAAAAAAAAAGCCCTTTTCAGTTTGTG	1187
Qy	3244	CACTGTGTACGGTCTGTGTAGGTTGATGCAGATTTTCTGAAATGAAA----TGTTTAGAC	3299
Db	1188	CACTGTGTATGGTCCGTGTAGATTGATGCAGATTTTCTGAAATGAAATGTTTGTTAGAC	1247
Qy	3300	GAGATCATGCCACCAAGGCAGGAGTGAAAAAGCTTGCCTTTCTGGTATGTTCTAGGTGT	3359
Db	1248	GAGATCATACCGGTAAAGCAGGAATGACAAAGCTTG-CTTTCTGGTATGTTCTAGGTGT	1306

Qy	3360	ATTGTGAAATTTACTGTTGTATTAAATGCCAATATAAGTAAATATAGATTATATATATCT	3419
Db	1307	ATTGTGACTTTTACTGTTATATTAATTGCCAATATAAGTAAATATAGATTATATATG---	1363
Qy	3420	ATATATAGTGT TTCACGAAGCTTAGCCCTTTACCTTCCCAGCTGCCCCACAGTGCTTGAT	3479
Db	1364	---TATAGTGT TTCACAAAGCTTAGACCTTTACCTT-CCAGCCACCCACAGTGCTTGAT	1419
Qy	3480	ACT-----TCTGTCATGGGTTTTATGTGTGTAGTCCCAAAGCACATAAGCTAGGGAGAA	3533
Db	1420	ATTTCAGAGTCAGTCATTGGTTATACATGTGTAGTTCCAAAGCACATAAGCTAGAAGAAG	1479
Qy	3534	ACGTACTTCTAGGCGCACTACCATCTGTTTTCAACACGAACCGACGCCATGCAAACAGAA	3593
Db	1480	AAATATTTCTAGGAGCACTACCATCTGTTTTCAACATGAA--ATGCCACACACATAGAA	1536
Qy	3594	CTCC-TCAACATAAACTTCAC TGACAGACTTACTGTAGTTAATTTTATCACAAACTCT-	3651
Db	1537	CTCCAACAACATCAATTTCA TTGCACAGACTGACTGTAGTTAATTTTGTACAGAATCTA	1596
Qy	3652	GGACTGAATCTAATGCTTCCAAA-----ATGTTTGCAAATATCAAACATTGTTATGTAAG	3707
Db	1597	TGGCTGAATCTAATGCTCCAAAATGTTGTTTGTGCAAATACCAACATTGTTATGCCAG	1656
Qy	3708	AAAATATA	3715
Db	1657	AAATTTTA	1664

RESULT 3

AK034902

LOCUS	AK034902	3533 bp	mRNA	linear	HTC 18-SEP-2003
DEFINITION	Mus musculus 12 days embryo embryonic body between diaphragm region and neck cDNA, RIKEN full-length enriched library, clone:9430059L06 product:RETICULON 4 (NEURITE OUTGROWTH INHIBITOR) (NOGO PROTEIN) (FOOCEN) [GLUT4 VESICLE 20 KDA PROTEIN] homolog [Rattus norvegicus], full insert sequence.				

ACCESSION AK034902

VERSION AK034902.1 GI:26084268

KEYWORDS HTC: CAP trapper.

SOURCE *Mus musculus* (house mouse)

ORGANISM *Mus musculus*

Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi;

Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae: Murinae: Mus.

REFERENCE 1

REFERENCE	1
AUTHORS	Carninci, P. and Hayashizaki, Y.

TITLE High-efficiency full-length cDNA cloning

JOURNAL Meth. Enzymol. 303: 19-44 (1999)

MEDLINE 00279253

MEDLINE	99279299
PUBMED	10349636

FORMED	10349030
REFERENCE	2

REFERENCE	Z
AUTHORS	Gannings, R. Shibata, Y. Hayatsu, N. Sugahara, Y. Shibata, K.

Authors: CAHILL, P. J., SHIBATA, T., HAYASHI, N., SAGANUMA, T., SHIBATA, K.,
Itah, M., Kanno, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.

TITLE Normalization and subtraction of car transporter selected cDNAs to

TITLE Normalization and subtraction of cap-trapper-selected cDNAs to
genomic full-length cDNA libraries for rapid discovery of new genes

prepare full-length cDNA libraries for rapid discovery of new genes

JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
 MEDLINE 88148874

PUBMED 11042159
 REFERENCE 3
 AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
 Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
 Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
 Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
 Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
 Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
 Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
 TITLE RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multicapillary sequencer
 JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
 MEDLINE 20530913
 PUBMED 11076861
 REFERENCE 4
 AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the
 FANTOM Consortium.
 TITLE Functional annotation of a full-length mouse cDNA collection
 JOURNAL Nature 409, 685-690 (2001)
 REFERENCE 5
 AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research
 Group Phase I & II Team.
 TITLE Analysis of the mouse transcriptome based on functional annotation
 of 60,770 full-length cDNAs
 JOURNAL Nature 420, 563-573 (2002)
 REFERENCE 6 (bases 1 to 3533)
 AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
 Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
 Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
 Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
 Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
 Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
 Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,
 Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
 Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
 Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
 Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
 Muramatsu,M. and Hayashizaki,Y.
 TITLE Direct Submission
 JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
 Physical and Chemical Research (RIKEN), Laboratory for Genome
 Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
 RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
 Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
 URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
 Fax:81-45-503-9216)
 COMMENT cDNA library was prepared and sequenced in Mouse Genome
 Encyclopedia Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues.
 Please visit our web site for further details.
 URL:http://genome.gsc.riken.go.jp/
 URL:http://fantom.gsc.riken.go.jp/.
 FEATURES Location/Qualifiers
 source 1. .3533
 /organism="Mus musculus"

Qy	2844	CCTGGATTGAAGCGTAAAGCTGAATGAGAAAAGCCTGAAAAGAGTTAAACAATAGAGGAGTTT	2903
Db	1280	 CCTGGATTGAAGCGCAAAGCAGAATGAAAAGGCCCAACAGTAGACA-----TTC	1330
Qy	2904	ATCTTTAAAGGGGATATTCATTTGATTCCATTG-GGGAGGGTCAGGGAAGAACAAAGCCT	2962
Db	1331	 ATCTTTAAAGGGGACACTCCCTTGGTTACGGGGTGGGCGGGTCAGGGGTGAGCCCTGGGT	1390
Qy	2963	TGACATTGCAGTGCAGTTTCACAGATCTTTATTTTTCAGCAACGCAGTGTCTGAGGAAAAA	3022
Db	1391	 GGCCGTGCAGTTTCAG-----TTATTTTTCAGTGCAGTGTCTGAGGAAAAA	1438
Qy	3023	TGACCTGTCTTGACTGCCCTGTGTTTCATCATCTTAAGTATTGTAAGCTGCTATGTATGGA	3082
Db	1439	 TTACCTGTCTTGACT-TCCTGTGTTTATCATCTTAAGTATTGTAAGCTGCTGTGTATGGA	1497
Qy	3083	TTTAAATCGTAATCATATTTGTTTTTCCCTGTATGAGGCAGTGGTGAATAAACAAAGATCT	3142
Db	1498	 TCT-CATTGTAGTCATACTTGTTTTCCCGAGATGAGGCAGTGGTGAATAAAGGATG-CT	1555
Qy	3143	GAGAAAGCTGTATATTACACTTTGTGCGCAGGTAGTCTTGCTGTATTTGGGGAATTGCAA	3202
Db	1556	 GGGAAAACTGTGTGTTATATTCTGTTGCAGGTAGTCTGGCTGTATTTGGAAAGTTGCAA	1615
Qy	3203	GAAAGTGGA----GCTGACAGAAATAACCCTTTTACAGTTTGTGCACTGTGTACGGTCT	3258
Db	1616	 GAAGGTAGATTTGGGGCAGGAAAAACAACCCTTTTACAGTGTACTGTGTTTGGTTGGT	1675
Qy	3259	GTGTAGGTTGATGCAGATTTTCTGAAATGAAATGTTTAGACGAGATCATGCCACCAAGGC	3318
Db	1676	 GTAAAACTGATGCAGATTTTCTGAAATGAGATGTTTAGATGAG--CATACTACTAAAGC	1733
Qy	3319	AGGAGTGAAAAAGCTTGCCTTTCCCTGGTATGTTCTAGGTGTATTGTGAAATTTACTGTTG	3378
Db	1734	 AGAGTGGAATACTGTC--TTTATGGTATGTTCTAGGTGTATTGTGATTTACTGT----	1787
Qy	3379	TATTAATTGCCAATATAAGTAAATATAGATTATATATATCTATATATAGTGTTCACGAA	3438
Db	1788	 --TAGATTGCCAATATAAGTAAATATAGA----CATAATCTATATATAGTGTTCACAAA	1841
Qy	3439	GCTTAGCCCTTTACCTTCCCAGCTGCCCCACAGTGCTTGATACTTCTGTCTATGGGTTTTA	3498
Db	1842	 GCTTAGATCTTTAACCTTGCAGCTGCCCCACAGTGCTTGACCTCTGAGTCATTGGTTATA	1901
Qy	3499	TGTGTGTAGTCCCAAAGCACATAAGCTAGGGAGAAACGTACTTCTAGGCGCACTACCATC	3558
Db	1902	 -CAGTGTAGTCCCAAGCACATAAACTAGGAAGAGAATGTATTTGTAGGAGCGCTACCACC	1960
Qy	3559	TGTTTTCAACACGAACCGACGCCATGCAAACAGAACTCCTCAACATAAACTTCACTGCAC	3618
Db	1961	 TGTTTTCAA-----GAGAACATAGAACTCCAACGTAACCGTCATTTCAA	2004
Qy	3619	AGACTTACTGTAGTTAATTTTATCACAACTCTGGACTGAATCTAATGCTTCCAAAAATG	3678
Db	2005	 AGATTTACTGTATGTA----TAGTTGATTTTGTGGACTGAATTTAATGCTTCC--AAATG	2058
Qy	3679	TTTGCAATATCAAACATTGTTATGTAAGAAAATAT-AAATGACGATTTATACAATTGTG	3737

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          |||||  || |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      2059 TTTGCAGTTACCAAACATTGTTATGCAAGAAATCATAAAATGAAGACTTATACCATGT- 2117

Qy      3738 GTTTAAGCTGTATTGAACTAAATCTGTGGAATGCATTGTGAACTGTAAAAGCAAAGTATC 3797
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      2118 GTTTAAGCTGTATTGAATT--ATCTGTGGAATGCATTGTGAACTGT-AAAGCAAAGTATC 2174

Qy      3798 AATAAAGCTTATAGACTTA 3816
          |||||  |||||  |||||  |||||
Db      2175 AATAAAGCTTATAGACTTA 2193

```

RESULT 4

AL573494/c

LOCUS AL573494 956 bp mRNA linear EST 31-MAY-2003

DEFINITION AL573494 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CS0DI051YB11 3-PRIME, mRNA sequence.

ACCESSION AL573494

VERSION AL573494.2 GI:31294840

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 956)

AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished (2001)

COMMENT On Feb 16, 2001 this sequence version replaced gi:12932794.

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 1423.r For more information about this cluster, see

<http://www.genoscope.cns.fr/>

[cgi-bin/cluster.cgi?seq=CS0DI051CA06NP1&cluster=1423.r](http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0DI051CA06NP1&cluster=1423.r). Contact :

Feng Liang Email : fliang@lifetech.com URL :

<http://fulllength.invitrogen.com/> InVitroGen Corporation 1600

Faraday Avenue Genoscope sequence ID : CS0DI051CA06NP1.

FEATURES

source

Location/Qualifiers

1. .956

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CS0DI051YB11"

/tissue_type="PLACENTA COT 25-NORMALIZED"

/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"

/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was

digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 17.4%; Score 668.6; DB 9; Length 956;

Best Local Similarity 88.7%; Pred. No. 1.5e-111;

Matches 795; Conservative 3; Mismatches 67; Indels 31; Gaps 6;

Qy	2304	GTTGTTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGC	2363
Db	878	GTTGTTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGC	819
Qy	2364	TTGTTCTGCTGCTCTCGCTGACAGTATTCAGCATTGTGAGTGTAACGGCCTACATTGCC	2423
		:	
Db	818	CTATTCCTGCTGCTTTTCATTRACAGTATTCAGCATTGTGAGCGTAACAGCCTACATTGCC	759
Qy	2424	TTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAAGGGTGTGATCCAGGCTATC	2483
Db	758	TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC	699
Qy	2484	CAGAAATCTGATGAAGGCCACCCATTCAGGGCATATTTGGAATCTGAAGTTGCTATATCT	2543
Db	698	CAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGAAGTTGCTATATCT	639
Qy	2544	GAGGAGTTGGTTCAGAAGTACAGCAATTCTGCTCTTGGTCATGTAACTGCACAATAAAA	2603
Db	638	GAGGAGTTGGTTCAGAAGTACAGTAATTCTGCTCTTGGTCATGTGAAGTGCACGATAAAG	579
Qy	2604	GAAGTCAGACGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTG	2663
Db	578	GAAGTCAGGCGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTG	519
Qy	2664	ATGTGGGTATTTACCTATGTTGGTGCCTTGTTCAATGGTCTGACACTACTAATTTTGGCT	2723
Db	518	ATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAAATGGTCTGACACTACTGATTTTGGCT	459
Qy	2724	CTGATTTCACTCTTCAGTGTTCTGTTATTTATGAACGGCATCAGGCGCAAATAGATCAT	2783
Db	458	CTCATTTCACTCTTCAGTGTTCTGTTATTTATGAACGGCATCAGGCACAGATAGATCAT	399
Qy	2784	TATCTGGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATC	2843
Db	398	TATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATC	339
Qy	2844	CCTGGATTGAAGCGTAAAGCTGAATGAGAAAGCCTGAAAGAGTTAACAATAGAGGAGTTT	2903
Db	338	CCTGGATTGAAGCGCAAAGCTGAATGAAAACGCCCAAATAATTA-----GTAGGAGTTC	284
Qy	2904	ATCTTTAAAGGGGATATTCATTTGATTCCATTGGGGAGGGTCAGGGAAGAACAAGCCTT	2963
Db	283	ATCTTTAAAGGGGATATTCATTTGATTATACGGGGAGGGTCAGGGAAGAACGAA-CCTT	225
Qy	2964	GACATTGCAGTGCAGTTTCAC-----AGATCTTTATTTTATAGCAACGCAGTG-T	3011
Db	224	GACGTTGCAGTGCAGTTTCACAGATCGTTGTTAGATCTTTATTTTATGCCATGCACTGTT	165
Qy	3012	CTGAGGAAAAATGACCTGTCTTGACTGCCCTGTGTTTCATCATCTTAAGTATTGTAAGCTG	3071
Db	164	GTGAGGAAAAATTACCTGTCTTTACTGCCATGTGTTTCATCATCTTAAGTATTGTAAGCTG	105
Qy	3072	CTATGTATGGATTTAAATCGTAATCATATTTGTTTTCTGTATGAGGCACTGGTGAATA	3131
Db	104	CTATGTATGGATTTAAACCGYAATCATA--TCTTTTCTATCTGAGGCACTGGTGA--	49

Qy 3132 AACAAAGATCTGAGAAAGCTGTATATTACACTTTGTCGCAGGTAGTCTTGCTGTAT 3187
 | | | | | | | | | | | | | | | | | | : |
 Db 48 -----ATAAAAAACCTGNANATTNNNACTTGTTCGCAGATAGTCTGGCCGCMT 2

RESULT 5

CB204418

LOCUS CB204418 896 bp mRNA linear EST 05-FEB-2003

DEFINITION AGENCOURT_11276017 NIH_MGC_135 Mus musculus cDNA clone
 IMAGE:30138586 5', mRNA sequence.

ACCESSION CB204418

VERSION CB204418.1 GI:28241848

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 896)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. David Rowe

cDNA Library Preparation: Invitrogen Corp

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: NDAM0041 row: k column: 11

High quality sequence stop: 686.

FEATURES

Location/Qualifiers

source

1. .896

/organism="Mus musculus"

/mol_type="mRNA"

/db_xref="taxon:10090"

/clone="IMAGE:30138586"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH_MGC_135"

/note="Vector: pCMVSPORT6.1; Site_1: EcoRV; Site_2: NotI;
 Normalized full-length enriched library from pooled mouse
 embryonic limb, maxilla and mandible, day 12.5, 13.5,
 14.5, and 15.5 (size selected for the 0.5-1 kb fragments)
 Cloned directionally, priming method: Oligo-dT. cDNA
 enrichment: >1k bp, Average insert size 1.6k bp.
 Normalization (Cot value): 7.5 kb. Priming sequence:
 5'GACTAGTTCTAGATCGCGAGCGGCCGCC(T)3' Tissue contributed
 by, David Rowe. Library constructed by ResGen, Invitrogen
 Corp."

ORIGIN

Query Match 16.9%; Score 646.8; DB 14; Length 896;

Best Local Similarity 85.3%; Pred. No. 1.4e-107;

Matches 761; Conservative 0; Mismatches 117; Indels 14; Gaps 3;

Qy	1856	AAGAGAAAGTGAAACATTTTCAGATTTCATCTCCGATTGAGATTATAGATGAGTTCCCAC	1915
Db	1	ATGAAAGAAGTGAACATTTTCGATTTCATCTCCATTGAGATAATAGATGAGTTCCCAC	60
Qy	1916	CTTTGTCAGTTCTAAAGCAGATTCTTCTCCTACATTAGCCAGGGAATACACTGACCTAGA	1975
Db	61	ATTTGTCAGTGCTAAAGATGATTCTCCT-----AAGGAGTACACTGACCTAGA	108
Qy	1976	AGTAGCCACAAAAAGTGAAATTGCTGACATCCAGGATGGAGCTGGGTTCATTGGCTTGTGC	2035
Db	109	AGTATCCAACAAAAGTGAAATTGCTAATGTCCAGAGCGGGCCAATTGCTTGCCTTGCTC	168
Qy	2036	AGGATTGCCCCATGACCTTTCTTTCAAGAGTATACAACCTAAAGAGGAAGTTCATGTCCC	2095
Db	169	AGAATTGCCCTGTGACCTTTCTTTCAAGAATACATATCCTAAAGATGAAGCACATGTCTC	228
Qy	2096	AGATGAGTTCTCCAAAGATAGGGGTGATGTTTCAAAGGTGCCCCGTACTGCCTCCAGATGT	2155
Db	229	AGATGAATTCTCCAAAGTAGGTCCAGTGTATCTAAGGTGCCCTTATTGCTTCCAAATGT	288
Qy	2156	TTCTGCTTTGGATGCTCAAGCAGAGATAGGCAGCATAGAAAAACCCAAAGTTCTTGTGAA	2215
Db	289	TTCTGCTTTGGAATCTCAAATAGAAATGGGCAACATAGTTAAACCCAAAGTACTTACGAA	348
Qy	2216	AGAAGCCGAGAGAAAACTTCCTTCTGATACAGAAAAAGAGCGAAGATCTCCATCTGCTAT	2275
Db	349	AGAAGCAGAGGAAAACTTCCTTCTGATACAGAGAAAGAGGACAGATCCCTGACAGCTGT	408
Qy	2276	ATTTTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAA	2335
Db	409	ATTGTCAGCAGAGCTGAATAAACTTCAGTTGTTGACCTCCTGTACTGGAGAGACATTAA	468
Qy	2336	GAAGACTGGAGTGGTGTGTTGGTGCCAGCTTGTTTCCTGCTGCTCTCGCTGACAGTATTAG	2395
Db	469	GAAGACTGGAGTGGTGTGTTGGTGCCAGCTTATTTCCTGCTGCTGTCTCTGACAGTGTTCAG	528
Qy	2396	CATTGTGAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCTGTGACTATCAGCTTTAG	2455
Db	529	CATTGTCAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCTGTGACTATCAGCTTTAG	588
Qy	2456	GATATATAAGGGTGTGATCCAGGCTATCCAGAAATCTGATGAAGGCCACCCATTAGGGC	2515
Db	589	GATATATAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTAGGGC	648
Qy	2516	ATATTTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTTCAAGTACAGCAATTCTGC	2575
Db	649	ATATTTGGAATCTGAAGTTGCCATATCAGAGGAATTGGTTTCAAGTATAGTAATTCTGC	708
Qy	2576	TCTTGGTCATGTTAACTGCACAATAAAAGAACTCAGACGCCTCTTCTTAGTTGATGATTT	2635
Db	709	TCTTGGTCATGTGAACAGCACATAAAAGAAATTGAGGCGTCTCTTCTTAGTTGATGATTT	768
Qy	2636	AGTTGATTCTCTGAAGTTTGCAGTGTGATGTGGGTATTTACCTATGTTGGTGCC-TTGT	2694
Db	769	AGTTGATTCCCTGAAG-TTGCAGTGTGATGTGGGTATTTACTTACGTTGGTGCCTTTGT	827
Qy	2695	TCAATGGTCTGACACTACTAATTTTGCTCTGATTTCACTCTTCAGTGTTCC	2746

Db 828 TCAATGGTTTGACACTACTGATTTTAGCCCTGATCTCACTCTTCAGTATTCC 879

RESULT 6

CK231727

LOCUS	CK231727	1003 bp	mRNA	linear	EST 09-DEC-2003
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DEFINITION ILLUMIGEN_MCQ_2869 Katze_MMBR Macaca mulatta cDNA 5' similar to human RTN4 (Hs.436349), mRNA sequence.

ACCESSION CK231727

VERSION CK231727.1 GI:39638085

KEYWORDS EST.

SOURCE *Macaca mulatta* (rhesus monkey)

ORGANISM *Macaca mulatta*

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.

REFERENCE 1 (bases 1 to 1003)

AUTHORS Katze, M.G., Thomas, M., Korth, M., Iadonato, S.P. and Magness, C.L.

TITLE Large-scale Rhesus Macaque cDNA Sequencing

JOURNAL Unpublished (2003)

COMMENT Contact: C. Magness

Illumigen Biosciences Inc.

2203 Airport Way S, Suite 450, Seattle, WA 98134, USA

Tel: 2063780400

Fax: 2063780408

Email: cmagness@illumigen.com

Sequenced on 2003.11.24. 765 Q20 bases. Assembles in contig w/ 2 member(s). Contig contains 1 (1.5%) lib members.

PCR PRImers

FORWARD: CCCTCACTAAAGGGGAACAAAA

BACKWARD: CACTATAGGGCGAATTGGGTA

Insert Length: 1003 Std Error: 0.00

Plate: CL000026 row: D column: 03

Seq primer: CCCTCACTAAAGGGAACAAAA

POLYA=No.

FEATURES	Location/Qualifiers
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source

1. .1003

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/organism="Macaca mulatta"
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/mol type="mRNA"
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/strain="Indian"

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/db xref="taxon:9544"
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/sex="female"
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/dev stage="adult"
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/lab host="E. coli SOLR"
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/clone lib="Katze MMBR"
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/note="Organ: brain; Vector: Uni-ZAP XR; Site_1: EcoR I;  
Site_2: Xho I; Created from Stratagene ZAP-cDNA Synthesis  
kit (catalog #200400) and ZAP-CDNA Gigapack III Gold  
Cloning Kit (Catalog #200450)"
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ORIGIN

Query Match 16.7%; Score 642; DB 14; Length 1003;

Best Local Similarity 84.1%; Pred. No. 1e-106;

Matches 853; Conservative 0; Mismatches 125; Indels 36; Gaps 10;

Qy 2469 GTGATCCAGGCTATCCAGAAATCTGATGAAGGCCACCCATT CAGGGCATATTTGGAATCT 2528

Db	9	GAGATCCAAGCTATCCAGAAATCAGATGAAGGCCCCCATTCAGGGCATATCTGGAATCT	68
Qy	2529	GAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGCAATTCTGCTCTTGGTCATGTT	2588
Db	69	GAAGTTGCGATATCTGAGGAGTTGGTTCAGAAGTACAGTAATTCTGCTCTTGGTCATGTG	128
Qy	2589	AACTGCACAATAAAAGAACTCAGACGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTG	2648
Db	129	AACTGCACGATAAAGGAACCTCAGGCGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTG	188
Qy	2649	AAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTCAATGGTCTGACA	2708
Db	189	AAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAATGGTCTGACG	248
Qy	2709	CTACTAATTTTGGCTCTGATTTCACTCTTCAGTGTTCTGTTATTTATGAACGGCATCAG	2768
Db	249	CTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTTCTGTTATTTATGAACGGCATCAG	308
Qy	2769	GCGCAAATAGATCATTATCTGGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAA	2828
Db	309	GCACAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAA	368
Qy	2829	ATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGAATGAGAAAGCCTGAAAGAGTTA	2888
Db	369	ATCCAAGCGAAAATCCCTGGATTGAAGCGCAAAGCTGAATGAAAACACCCAAAATAATTA	428
Qy	2889	ACAATAGAGGAGTTTATCTTTAAAGGGGATATTCATTTGATTCCATTGGGGAGGGTCAGG	2948
Db	429	-----CTAGGAGTTCATCTTTAAAGGGGTATTCATTTGAGTATATGGGGAGGGTCAGG	483
Qy	2949	GAAGAACAAAGCCTTGACATTGCAGTGCAGTTTTCAC-----AGATCTTTATTTT	2997
Db	484	GAAGAACGAA-CCTTGACATTGCAGTGCAGTTTTCACAGATCGTTGTTAGATCTTTATTTT	542
Qy	2998	TAGCAACGCAGTG-TCTGAGGAAAAATGACCTGTCTTGACTGCCCTGTGTTTCATCATCTT	3056
Db	543	TAGCCATGCACTGTTGTGAGGGAAAATTACCTGTCTTGACTGCCATGTGTTTCATCATC-T	601
Qy	3057	AAGTATTGTAAGCTGCTATGTATGGATTAAATCGTAATCATATTTGTTTTTCTGTATG	3116
Db	602	AAGTATTGTAAGCTGCTATGTATGGATTAAACCGTAATCATA--TCTTTTTCTATCTG	659
Qy	3117	AGGCACTGGTGAATAAACAAGATCTGAGAAAGCTGTATATTACACTTTGTGCGAGGTAG	3176
Db	660	AGGCACTGGTGGA-----ATAAAAAACCTGTATATTTTACTTTGTTGCAGGTAG	708
Qy	3177	TCTTGCTGTAT-TTGGGGAATTGCAAAGAAAGTGGAGCTGACAGAAATAACCCTTTTTCAC	3235
Db	709	TCTTGCTGCATCTTGGAAGTTGCAGAGATGGTGGAGTTAGAAAAAAGCCCTTTT--C	766
Qy	3236	AGTTTGTGCACTGTGTACGGTCTGTGTAGGTTGATGCAGATTTTCTGAAATGAAATGTTT	3295
Db	767	AGTTTGTGCACTGTGTATGGTCCGTGTAGATTGATGCAGATTTTCTGAAATGAAATGTTT	826
Qy	3296	AGACGAGATCATGCCACCAAGGCAGGAGTGAAAAAGCTTGCCTTTCTGGTATGTTCTAG	3355


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Db      760 GAATAAAGGA--CTCGGGGAAAGCTGTGCATTGTATCTGCTGCAGGGTAGTCTAGCTGTA 817
Qy      3187 TTTGGGGAATTGCAAAGAAAGTGGAGCT---GACAGAAATAACCCCTTTTCACAGTTTGTG 3243
      | | | | | ||||| | | | | | | | | | | | | | | |
Db      818 TGCAGAGAGTTGTAAAGAAGGCAAATCTGGGGGCAGGGAAAACCCCTTTTCACAG--TGTA 875
Qy      3244 CACTGTGTACGGTCTGTGTAGGTTGATGCAGATTTTCTGAAATGAAATGTTTAGACGAGA 3303
      | ||| | | | | | | | | | | | | | | | | | | | |
Db      876 CTGTGTTTGGTCAGTGTA AAACTGATGCAGATTTTCTGAAATGAAATGTTTAGATGAGA 935
Qy      3304 TCATGCCACCAAGGCAGGAGTGAAAAAGCTTGCCTTTCTGGTATGTTCTAGGTGTATTG 3363
      ||| | | | | | | | | | | | | | | | | | | | |
Db      936 GCATACTACTAAAGCAGAGTGGA AAACTCTGTC--TTTATGGTGTGTTCTAGGTGTATTG 993
Qy      3364 TGAAATTTACTGTTGTATTAATTGCCAATATAAGTAAATATAGATTATATATATCTATAT 3423
      || ||||| ||||| | | | | | | | | | | | | | | |
Db      994 TG-AATTTACTGTTAT----ATTGCCAATATAAGTAAATATAGA----CCTAATCTATAT 1044
Qy      3424 ATAGTGTTTCACGAAGCTTAGCCCTTTACCTTCCCAGCTGCCCCACAGTGCTTGA 3478
      ||||| ||||| ||||| | | | | | | | | | | | | |
Db      1045 ATAGTGTTTCACAAAGCTTAGATCTTTAACCTTGCAGCTGCCCCACAGTGCTTGA 1099

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RESULT 8

BQ719894

LOCUS BQ719894 871 bp mRNA linear EST 16-JUL-2002

DEFINITION AGENCOURT_8241298 Lupski_sympathetic_trunk Homo sapiens cDNA clone
IMAGE:6187240 5', mRNA sequence.

ACCESSION BQ719894

VERSION BQ719894.1 GI:21858791

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 871)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. James R. Lupski

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM13580 row: o column: 17

High quality sequence stop: 677.

FEATURES

source

Location/Qualifiers

1. .871

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:6187240"


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/sex="male"
/tissue_type="sympathetic trunk"
/dev_stage="adult, 16 yr"
/lab_host="DH10B"
/clone_lib="Lupski_sympathetic_trunk"
/note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
NotI; Site_2: SalI; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TCGACCCACGCGTCCG-3' and
5'-GACTAGTTCTAGATCGCGAGCGGCCCT(15)-3'. Size selected >
1 kb for average insert length 1.9 kb. This is a primary
library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
College of Medicine); available through Life
Technologies."

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ORIGIN

```

Query Match          16.5%; Score 631; DB 13; Length 871;
Best Local Similarity 86.2%; Pred. No. 1e-104;
Matches 731; Conservative 0; Mismatches 110; Indels 7; Gaps 3;

Qy      909 GAGGAAGTAGTGGCAAACATGCCTGAAGGTCTAACCCAGATTTGGTTCAGGAAGCATGT 968
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      11  GCGGACGCGTGGGCAAACATGCCTGAAGGCCTGACTCCAGATTTAGTACAGGAAGCATGT 70

Qy      969 GAAAGTGAATTGAATGAAGCTACTGGTACAAAAATTGCCTTTGAAACAAAAATGGACCTG 1028
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      71  GAAAGTGAATTGAATGAAGTTACTGGTACAAAGATTGCTTATGAAACAAAAATGGACTTG 130

Qy     1029 GTTCAAACCTTCAGAAGCTGTGCAGGAGTCACTTTACCCTGTAACACAGCTTTGCCCATCT 1088
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     131  GTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCACAGCTTTGCCCATCA 190

Qy     1089 TTTGAAGAATCTGAAGCTACTCCGTCACCGGTTTTGCCTGACATTGTCATGGAAGCACCA 1148
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     191  TTTGAAGAGTCAGAAGCTACTCCTTCACAGTTTTGCCTGACATTGTTATGGAAGCACCA 250

Qy     1149 TTAAATTCTGTAGTTCCTAGTGCTGGTGCTTCTGCAGTGCAGCTCAGTTCATCACCATTA 1208
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     251  TTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGATACAGCCCAGCTCATCACCATTA 310

Qy     1209 GAAACTCTTCCTTCAGTTAATTATGAAAGCATAAAGTTTGAGCCTGAAAATCCCCCACCA 1268
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     311  GAAGC---TTCTTCAGTTAATTATGAAAGCATAAAACATGAGCCTGAAAACCCCCCACCA 367

Qy     1269 TATGAGGAGGCCATGAATGTATCACTAAAAAAGAATCAGGAATGAATGAAGAAATCACA 1328
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     368  TATGAAGAGGCCATGAGTGTATCACTAAAAAAGTATCAGGAATAAAGGAAGAAATTAA 427

Qy     1329 GAGCCTGAAGGTATTAGTGTAGCTGTTTCAGGAAACAGAAGCTCCTTATATATCTATTGCA 1388
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     428  GAGCCTGAAAATATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTATATATCTATTGCA 487

Qy     1389 TGTGATTTAATTAAAGAAACAAAGATCTCTACTGAACCGACTCCAGATTTCTCTAGTTAT 1448
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     488  TGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAACCGACTCCGATTTCTCTGATTAT 547

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LOCUS       CB467517                          646 bp      mRNA      linear      EST 26-MAR-2003
DEFINITION  733269 MARC 6BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION   CB467517
VERSION     CB467517.1  GI:29273902
KEYWORDS    EST.
SOURCE      Bos taurus (cow)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
            Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 646)
  AUTHORS   Smith,T.P.L., Roberts,A.J., Echternkamp,S.E., Chitko-McKown,C.G.,
            Wray,J.E. and Keele,J.W.
  TITLE     A second set of bovine ESTs from pooled-tissue normalized libraries
  JOURNAL    Unpublished (2003)
COMMENT     Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called with phred v0.020425.c and
            trimmed with the aid of the trim_alt option. Vector identified with
            cross_match v0.990329.
            Plate: LAM8011 row: E column: 7
            Seq primer: GTAATACGACTCACTATAGGG.
FEATURES             Location/Qualifiers
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                       /organism="Bos taurus"
                       /mol type="mRNA"

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/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARC 6BOV"
/note="Vector: pcDNA3.1; Site_1: EcoRI; Site_2: NotI;
Library made with RNA pooled from multiple tissues
including liver, lung, hypothalamus, pituitary, and
placenta/endometrium."

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ORIGIN

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Query Match          16.4%;  Score 628.8;  DB 14;  Length 646;
Best Local Similarity 99.4%;  Pred. No. 2.9e-104;
Matches 642;  Conservative 0;  Mismatches 2;  Indels 2;  Gaps 1;

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Qy      3177 TCTTGCTGTATTTGGGGAATTGCAAAGAAAGTGGAGCTGACAGAAATAACCCCTTTTCACA 3236
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Db       1   TCTTGCTGTATTTGGGGAATTGCAAAGAAAGTGGAGCTGACAGAAATAACCCCTTTTCACA 60

Qy      3237 GTTTGTGCACTGTGTACGGTCTGTGTAGGTTGATGCAGATTTTCTGAAATGAAATGTTTA 3296
          |||
Db       61  GTTTGTGCACTGTGTACGGTCTGTGTAGGTTGATGCAGATTTTCTGAAATGAAATGTTTA 120

Qy      3297 GACGAGATCATGCCACCAAGGCAGGAGTGAAAAAGCTTGCCCTTTCCTGGTATGTTCTAGG 3356
          |||
Db      121  GACGAGATCATGCCACCAAGGCAGGAGTGAAAAAGCTTGCCCTTTCCTGGTATGTTCTAGG 180

Qy      3357 TGTATTGTGAAATTTACTGTTGTATTAATTGCCAATATAAGTAAATATAGAT--TATATA 3414
          |||
Db      181  TGTATTGTGAAATTTACTGTTGTATTAATTGCCAATATAAGTAAATATAGATTATATATA 240

Qy      3415 TATCTATATATAGTGTTTCACGAAGCTTAGCCCTTTACCTTCCCAGCTGCCCCACAGTGC 3474
          |||
Db      241  TATCTATATATAGTGTTTCATGAAGCTTAGCCCTTTACCTTCCCAGCTGCCCCACAGTGC 300

Qy      3475 TTGATACTTCTGTCATGGGTTTTATGTGTGTAGTCCCAAAGCACATAAGCTAGGGAGAAA 3534
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Db      301  TTGATACTTCTGTCATGGGTTTTATGTGTGTAGTCCCAAAGCACATAAGCTAGGGAGAAA 360

Qy      3535 CGTACTTCTAGGCGCACTACCATCTGTTTTCAACACGAACCGACGCCATGCAAACAGAAC 3594
          |||
Db      361  CGTACTTCTAGGCGCACTACCATCTGTTTTCAACACGAACCGACGCCATGCAAACAGAAC 420

Qy      3595 TCCTCAACATAAACTTCACTGCACAGACTTACTGTAGTTAATTTTATCACAAACTCTGGA 3654
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Db      421  TCCTCAACATAAACTTCACTGCACAGACTTACTGTAGTTAATTTTATCACAAACTCTGGA 480

Qy      3655 CTGAATCTAATGCTTCCAAAAATGTTTGCAAATATCAAACATTGTTATGTAAGAAAATAT 3714
          |||
Db      481  CTGAATCTAATGCTTCCAAAAATGTTTGCAAATATCAAACATTGTTATGTAAGAAAATAT 540

Qy      3715 AAATGACGATTTATACAATTGTGGTTTAAAGCTGTATTGAACTAAATCTGTGGAATGCATT 3774
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Db      541  AAATGACGATTTATACAATTGTGGTTTAAAGCTGTATTGAACTAAATCTGTGGAATGCATT 600

Qy      3775 GTGAACTGTAAAAGCAAAGTATCAATAAAGCTTATAGACTTAAAAA 3820
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Db      601  GTGAACTGTAAAAGCAAAGTATCAATAAAGCTTATAGACCTAAAAA 646

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RESULT 10
 BM986175
 LOCUS BM986175 627 bp mRNA linear EST 22-MAR-2002
 DEFINITION LM24HW00149 Bos taurus LM-24-HW cDNA library Bos taurus cDNA clone
 LM-24-HW-001-49 (5'), mRNA sequence.
 ACCESSION BM986175
 VERSION BM986175.1 GI:19684841
 KEYWORDS EST.
 SOURCE Bos taurus (cow)
 ORGANISM Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 Bovidae; Bovinae; Bos.
 REFERENCE 1 (bases 1 to 627)
 AUTHORS Yoon,D.H., Jang,Y.S., Kim,T.H., Park,E.W., Lee,H.K., Chung,E.R.,
 Sun,S.S. and Cheong,I.C.
 TITLE Gene Expression Profiling of the Bovine skeletal muscle
 JOURNAL Unpublished (2002)
 COMMENT Contact: Dr. Du-Hak Yoon
 National Livestock Research Institute, RDA
 564 Omockchun-dong, Suwon, 441-350, Korea
 Tel: 82 31 290 1593
 Fax: 82 31 290 1792
 Email: dhyoon@rda.go.kr
 Insert Length: 839 Std Error: 0.00
 Seq primer: CAGGAAACAGCTATGAC
 POLYA=No.
 FEATURES Location/Qualifiers
 source 1..627
 /organism="Bos taurus"
 /mol_type="mRNA"
 /db_xref="taxon:9913"
 /clone="LM-24-HW-001-49 (5')"
 /sex="six males mixed"
 /tissue_type="longissimus dorsi"
 /cell_type="myocyte"
 /dev_stage="24 months old"
 /lab_host="XL1-BlueMRF'strain"
 /clone_lib="Bos taurus LM-24-HW cDNA library"
 /note="Organ: skeletal muscle; Vector: Uni-ZAPXR; Site_1:
 EcoRI; Site_2: Xho I"
 ORIGIN
 Query Match 16.3%; Score 625.4; DB 12; Length 627;
 Best Local Similarity 99.8%; Pred. No. 1.2e-103;
 Matches 626; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 2766 CAGGCGCAAATAGATCATTATCTGGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCT 2825
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 Db 1 CAGGCGCAAATAGATCATTATCTGGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCT 60
 Qy 2826 AAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGAATGAGAAAGCCTGAAAGAG 2885
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 61 AAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGAATGAGAAAGCCTGAAAGAG 120

Qy 2886 TTAACAATAGAGGAGTTTATCTTTAAAGGGGATATTCATTTGATTCCATTGGGGAGGGTC 2945
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 Db 121 TTAACAATAGAGGAGTTTATCTTTAAAGGGGATATTCATTTGATTCCATTGGGGAGGGTC 180
 Qy 2946 AGGGAAGAACAAGCCTTGACATTGCAGTGCAGTTTCACAGATCTTTATTTTATAGCAACG 3005
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 Db 181 AGGGAAGAACAAGCCTTGACATTGCAGTGCAGTTTCACAGATCTTTATTTTATAGCAACG 240
 Qy 3006 CAGTGTCTGAGGAAAAATGACCTGTCTTGACTGCCCTGTGTTTCATCATCTTAAGTATTGT 3065
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 Db 241 CAGTGTCTGAGGAAAAATGACCTGTCTTGACTGCCCTGTGTTTCATCATCTTAAGTATTGT 300
 Qy 3066 AAGCTGCTATGTATGGATTTAAATCGTAATCATATTTGTTTTCTGTATGAGGCACTGG 3125
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 Db 301 AAGCTGCTATGTATGGATTTAAATCGTAATCATATTTGTTTTCTGTATGAGGCACTGG 360
 Qy 3126 TGAATAAAACAAAGATCTGAGAAAGCTGTATATTACACTTTGTGCGCAGGTAGTCTTGCTGT 3185
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 Db 361 TGAATAAAACAAAGATCTGAGAAAGCTGTATATTACACTTTGTGCGCAGGTAGTCTTGCTGT 420
 Qy 3186 ATTTGGGGAATTGCAAAGAAAGTGGAGCTGACAGAAATAACCCCTTTTCACAGTTTGTGCA 3245
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 Db 421 ATTTGGGGAATTGCAAAGAAAGTGGAGCTGACAGAAATAACCCCTTTTCACAGTTTGTGCA 480
 Qy 3246 CTGTGTACGGTCTGTGTAGGTTGATGCAGATTTTCTGAAATGAAATGTTTAGACGAGATC 3305
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 Db 481 CTGTGTACGGTCTGTGTAGGTTGATGCAGATTTTCTGAAATGAAATGTTTAGACGAGATC 540
 Qy 3306 ATGCCACCAAGGCAGGAGTGAAAAAGCTTGCCTTTCTGGTATGTTCTAGGTGTATTGTG 3365
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 Db 541 ATGCCACCAAGGCAGGAGTGAAAAAGCTTGCCTTTCTGGTATGTTCTAGGTGTATTGTG 600
 Qy 3366 AAATTTACTGTTGTATTAATTGCCAAT 3392
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 Db 601 AAAATTACTGTTGTATTAATTGCCAAT 627

RESULT 11

BG570231

LOCUS BG570231 843 bp mRNA linear EST 10-APR-2001

DEFINITION 602590632F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4717662 5',
 mRNA sequence.

ACCESSION BG570231

VERSION BG570231.1 GI:13577884

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 843)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: CLONTECH Laboratories, Inc.

cDNA Library Preparation: CLONTECH Laboratories, Inc.

Db 362 ATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAAATGGTCTGACACTACTGATTTTGGCT 421
 Qy 2724 CTGATTTCACTCTTCAGTGTTCCTGTTATTTATGAACGGGCATCAGGCGCAAATAGATCAT 2783
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 Db 422 CTCATTTCACTCTTCAGTGTTCCTGTTATTTATGAACGGGCATCAGGCACAGATAGATCAT 481
 Qy 2784 TATCTGGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATC 2843
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 Db 482 TATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATC 541
 Qy 2844 CCTGGATTGAAGCGTAAAGCTGAATGAGAAAGCCTGAAAGAGTTAACAATAGAGGAGTTT 2903
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 Db 542 CCTGGATTGAAGCGCAAAGCTGAATGAAAACGCCCAAATAATTA-----GTAGGAGTTC 596
 Qy 2904 ATCTTTAAAGGGGATATTCATTTGATTCCATTGGGGAGGGTCAGGGAAGAACAAGCCTT 2963
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 Db 597 ATCTTTAAAGGGGATATCCATTTGATTATACGGGGGAGGGTCCAGGAAGAACGAACCTTG 656
 Qy 2964 GACATTGCAGTGCAGTTTCACAGAT-----CTTTATTTTATAGCAACGCAGTG-T 3011
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 Db 657 ACGTTTGCAGTGCAGTTTCACAGATCGTAGTAGATCCTTTATTTTATAGCCCTGCACTGTT 716
 Qy 3012 CTGAGGAAAAATGACCTGTCTTGACT-GCCCTGTGTTTCATCATCTTAA-GTATTGTAAGC 3069
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 Db 717 GTGCAGGAAAATTACCTGTCTTGACTGGCCATGTTGTCATCATCTTAAGGTATTGTAAGC 776
 Qy 3070 TGCTATGTATGGATTTAAATCGTAATCATATTTGTTTTCTGTATGAGGCACTGGTGAA 3129
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 Db 777 TGCTATGTATGGATTTAAACCGTATCATATCTTTTCTATCTAATCTGAGGACTGTGGAA 836
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 Db 837 TTAAAAA 843

RESULT 12

CF768055

LOCUS CF768055 619 bp mRNA linear EST 17-OCT-2003

DEFINITION CES004952 Bos taurus skin cDNA library Bos taurus cDNA clone
CCL004952 5', mRNA sequence.

ACCESSION CF768055

VERSION CF768055.1 GI:37717274

KEYWORDS EST.

SOURCE Bos taurus (cow)

ORGANISM Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.

REFERENCE 1 (bases 1 to 619)

AUTHORS Wang, Y.H., McWilliam, S. and Lehnert, S.

TITLE Transcription profiling of cattle skin

JOURNAL Unpublished (2003)

COMMENT Contact: Dr Yonghong Wang

Functional Genomics Lab

CSIRO Livestock Industries

Level 5, Queensland Biosciences Precinct, University of Queensland,

306 Carmody Road St. Lucia QLD Australia

Tel: 07 3214 2445
Fax: 07 3214 2685
Email: Yonghong.Wang@csiro.au
Plate: 6 row: D column: 10.

FEATURES
source Location/Qualifiers
1. .619
/organism="Bos taurus"
/mol_type="mRNA"
/strain="Hereford Shorthorn"
/db_xref="taxon:9913"
/clone="CCL004952"
/sex="female"
/tissue_type="pooled"
/dev_stage="Adult"
/lab_host="XL1-BlueMRF'strain"
/clone_lib="Bos taurus skin cDNA library"
/note="Organ: skin; Vector: Uni-ZAPXR; Site_1: EcoRI;
Site_2: Xho I; Library made from pooled skin of adult
female Hereford-Shorthorn."

ORIGIN

Query Match 16.1%; Score 619; DB 14; Length 619;
Best Local Similarity 100.0%; Pred. No. 1.7e-102;
Matches 619; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2507 ATTCAGGGCATATTTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAG 2566
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Db 1 ATTCAGGGCATATTTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAG 60

Qy 2567 CAATTCTGCTCTTGGTCATGTTAACTGCACAATAAAAGAACTCAGACGCCTCTTCTTAGT 2626
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Db 61 CAATTCTGCTCTTGGTCATGTTAACTGCACAATAAAAGAACTCAGACGCCTCTTCTTAGT 120

Qy 2627 TGATGATTTAGTTGATTCTCTGAAGTTTGCACTGTTGATGTGGGTATTTACCTATGTTGG 2686
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Db 121 TGATGATTTAGTTGATTCTCTGAAGTTTGCACTGTTGATGTGGGTATTTACCTATGTTGG 180

Qy 2687 TGCCTTGTTCAATGGTCTGACACTACTAATTTTGGCTCTGATTTCACTCTTCAGTGTTCC 2746
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Db 181 TGCCTTGTTCAATGGTCTGACACTACTAATTTTGGCTCTGATTTCACTCTTCAGTGTTCC 240

Qy 2747 TGTTATTTATGAACGGGCATCAGGCGCAAATAGATCATTATCTGGGACTTGCAAATAAGAA 2806
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Db 241 TGTTATTTATGAACGGGCATCAGGCGCAAATAGATCATTATCTGGGACTTGCAAATAAGAA 300

Qy 2807 TGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGA 2866
|
Db 301 TGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGA 360

Qy 2867 ATGAGAAAGCCTGAAAGAGTTAACAATAGAGGAGTTTATCTTTAAAGGGGATATTCATTT 2926
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Db 361 ATGAGAAAGCCTGAAAGAGTTAACAATAGAGGAGTTTATCTTTAAAGGGGATATTCATTT 420

Qy 2927 GATTCCATTGGGGAGGGTCAGGGAAGAACAAGCCTTGACATTGCAGTGCAGTTTCACAG 2986
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Qy 2987 ATCTTTATTTTATAGCAACGCAGTGTCTGAGGAAAAATGACCTGTCTTGACTGCCCTGTGT 3046
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 Db 481 ATCTTTATTTTATAGCAACGCAGTGTCTGAGGAAAAATGACCTGTCTTGACTGCCCTGTGT 540
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 Qy 3047 TCATCATCTTAAGTATTGTAAGCTGCTATGTATGGATTAAATCGTAATCATATTTGTTT 3106
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 Db 541 TCATCATCTTAAGTATTGTAAGCTGCTATGTATGGATTAAATCGTAATCATATTTGTTT 600
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 Qy 3107 TTCCTGTATGAGGCACTGG 3125
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 Db 601 TTCCTGTATGAGGCACTGG 619

RESULT 13

CK232009

LOCUS CK232009 1164 bp mRNA linear EST 09-DEC-2003

DEFINITION ILLUMIGEN_MCQ_3196 Katze_MMPL2 Macaca mulatta cDNA 5' similar to human RTN4 (Hs.436349), mRNA sequence.

ACCESSION CK232009

VERSION CK232009.1 GI:39638367

KEYWORDS EST.

SOURCE Macaca mulatta (rhesus monkey)

ORGANISM Macaca mulatta

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Cercopithecinae; Macaca.

REFERENCE 1 (bases 1 to 1164)

AUTHORS Katze,M.G., Thomas,M., Korth,M., Iadonato,S.P. and Magness,C.L.

TITLE Large-scale Rhesus Macaque cDNA Sequencing

JOURNAL Unpublished (2003)

COMMENT Contact: C. Magness

Illumigen Biosciences Inc.

2203 Airport Way S, Suite 450, Seattle, WA 98134, USA

Tel: 2063780400

Fax: 2063780408

Email: cmagness@illumigen.com

Sequenced on 2003.11.25. 797 Q20 bases. Assembles in contig w/ 2 member(s). Contig contains 1 (0%) lib members.

PCR Primers

FORWARD: CCCTCACTAAAGGGAACAAAA

BACKWARD: CACTATAGGGCGAATTGGGTA

Insert Length: 1164 Std Error: 0.00

Plate: CL000027 row: F column: 08

Seq primer: CCCTCACTAAAGGGAACAAAA

POLYA=No.

FEATURES

source

Location/Qualifiers

1. .1164

/organism="Macaca mulatta"

/mol_type="mRNA"

/strain="Indian"

/db_xref="taxon:9544"

/sex="male"

/dev_stage="newborn infant"

/lab_host="E. coli SOLR"

/clone_lib="Katze_MMPL2"

/note="Organ: placenta; Vector: Uni-ZAP XR; Site_1: EcoR I; Site_2: Xho I; Created from Stratagene ZAP-cDNA"

ORIGIN

Qy	2428	CCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAAGGGTGTGATCCAGGCTATCCAGA	2487
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Qy	2488	AATCTGATGAAGGCCACCCATTGAGGCGATATTTGGAATCTGAAGTTGCTATATCTGAGG	2547
Db	107	AATCAGATGAAGGCCACCCATTGAGGCGATATCTGGAATCTGAAGTTGCGATATCTGAGG	166
Qy	2548	AGTTGGTTTCAAGTACAGCAATTCTGCTCTTGGTCATGTAACTGCACAATAAAAGAAC	2607
Db	167	AGTTGGTTTCAAGTACAGTAATTCTGCTCTTGGTCATGTGAAGTGCACGATAAAGGAAC	226
Qy	2608	TCAGACGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTGATGT	2667
Db	227	TCAGGCGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTGATGT	286
Qy	2668	GGGTATTTACCTATGTTGGTGCCTTGTTCAATGGTCTGACACTACTAATTTTGGCTCTGA	2727
Db	287	GGGTATTTACCTATGTTGGTGCCTTGTTAATGGTCTGACGCTACTGATTTTGGCTCTCA	346
Qy	2728	TTTCACTCTTCAGTGTTTCTGTTATTTATGAAC-GGCATCAGGCGCAAATAGATCATTAT	2786
Db	347	TTTCACTCTTCAGTGTTTCTGTTATTTATGAACNGGCATCAGGCACAGATAGATCATTAT	406
Qy	2787	CTGGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCT	2846
Db	407	CTAGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCGAAAATCCCT	466
Qy	2847	GGATTGAAGCGTAAAGCTGAATGAGAAAGCCTGAAAGAGTTAACAATAGAGGAGTTTATC	2906
Db	467	GGATTGAAGCGCAAAGCTGAATGAAAACACCCAAAATAATTA-----CTAGGAGTTCATC	521
Qy	2907	TTTAAAGGGGATATTTCATTTGATTCCATTGGGGAGGGTCAGGGAAGAACAAAGCCTTGAC	2966
Db	522	TTTAAAGGGGGTATTTCATTTGAGTATATGGGGAGGGTCAGGGAAGAACGAA-CCTTGAC	580
Qy	2967	ATTGCAGTGCAGTTTCAC-----AGATCTTTATTTTTAGCAACGCAGTG-TCTG	3014
Db	581	ATTGCAGTGCAGTTTCACAGATCGTTGTTAGATCTTTATTTTTAGCCATGCACTGTTGTG	640
Qy	3015	AGGAAAAATGACCTGTCTTGACTGCCCTGTGTTTCATCATCTTAAGTATTGTAAGCTGCTA	3074
Db	641	AGGGAAAATTACCTGTCTTGACTGCCATGTGTTTCATCATC-TAAGTATTGTAAGCTGCTA	699
Qy	3075	TGTATGGATTTAAATCGTAATCATATTTGTTTTTCTGTATGAGGCACTGGTGAATAAAC	3134
Db	700	TGTATGGATTTAAACCGTAATCATA--TCTTTTTCTATCTGAGGCACTGGTGA-----	752
Qy	3135	AAAGATCTGAGAAAGCTGTATATTACACTTTGTGCGAGGTAGTCTTGCTGTAT-TTGGGG	3193

Db	753	-----ATAAAAAACCTGTATATTTTACTTTGTTGCAGGTAGTCTTGCTGCATCTTGGCA	806
Qy	3194	AATTGCAAAGAAAGTGGAGCTGACAGAAATAACCCTTTTACAGTTTGTGCACTGTGTAC	3253
Db	807	AGTTGCAGAGATGGTGGAGTTAGAAAAAAAAAGCCCTTT--CAGTTTGTGCACTGTGTAT	864
Qy	3254	GGT-CTGTGTAGGTTGATGCAGATTTTCTGAAATGAAATGTTTAGACGAGATCATGCCAC	3312
Db	865	GGTCCC GTGTAGATTGATGCAGATTTTCTGAAATGAAATGTTTAGACAAGATCATACCCA	924
Qy	3313	CAAGGCAGGAGTGAAAAAGCTTGCCTTTCCTGGTATGTTCTAGGTGTATTGTGAAATTTA	3372
Db	925	GTAAAGCAGGAATGAAAATCTTGCCTTTCCTGGTATGTTCTAGGGGTATTGGGACTTTTA	984
Qy	3373	CTGTTGTATTAATTGCCAAT-ATAAGTAAATATAGATTATATATATCTATATATAGTGTT	3431
Db	985	CTGGTATATTAATTGCCAATAATAAGTAAATATAAATTA----ATATAATATAAGTGTT	1039
Qy	3432	TCACGAAGCTT---AGCCCTTTACCTTCCCAGCTGCCCCAC	3469
Db	1040	TCCCCAAACTTTTAAACCTTTTACCTTTCAGCCCCCCCCC	1080

FORWARD: TAATACGACTCACTATAGGG
 BACKWARD: ATTAACCCCTCACTAAAG
 Insert Length: 631 Std Error: 0.00
 Plate: BP250021B10 row: D column: 3
 Seq primer: AGCGGATAACAATTCACACAGGA
 High quality sequence stop: 631.

FEATURES
 source Location/Qualifiers
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 /mol_type="mRNA"
 /db_xref="taxon:9913"
 /clone="BP250021B10D3"
 /sex="female"
 /lab_host="DH10B"
 /clone_lib="Soares normalized bovine placenta"
 /note="Organ: placenta; Vector: pT7T3Pac; Site_1: EcoRI;
 Site_2: NotI; The cDNA library was contributed by the
 Soares laboratory and it was constructed and normalized
 as described by Bonaldo, M.F., Lennon, G. and Soares,
 M.B. (1996), Genome Research 6(9): 791-806. "

ORIGIN

Query Match 16.1%; Score 617; DB 10; Length 631;
 Best Local Similarity 99.7%; Pred. No. 4e-102;
 Matches 629; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

Qy	2834	AGCAAAAATCCCTGGATTGAAGCGTAAAGCTGAATGAGAAAGCCTGAAAGAGTTAACAAT	2893
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Qy	2894	AGAGGAGTTTATCTTTAAAGGGGATATTCATTTGATTCCATTGGGGAGGGTCAGGGAAGA	2953
Db	61	AGAGGAGTTTATCTTTAAAGGGGATATTCATTTGATTCCATTGGGGAGGGTCAGGGAAGA	120
Qy	2954	ACAAAGCCTTGACATTGCAGTGCAGTTTCACAGATCTTTATTTTGTAGCAACGCAGTGTCT	3013
Db	121	ACAAAGCCTTGACATTGCAGTGCAGTTTCACAGATCTTTATTTTGTAGCAACGCAGTGTCT	180
Qy	3014	GAGGAAAAATGACCTGTCTTGACTGCCCTGTGTTTCATCATCTTAAGTATTGTAAGCTGCT	3073
Db	181	GAGGAAAAATGACCTGTCTTGACTGCCCTGTGTTTCATCATCTTAAGTATTGTAAGCTGCT	240
Qy	3074	ATGTATGGATTTAAATCGTAATCATATTTGTTTTTCCTGTATGAGGCACTGGTGAATAAA	3133
Db	241	ATGTATGGATTTAAATCGTAATCATATTTGTTTTTCCTGTATGAGGCACTGGTGAATAAA	300
Qy	3134	CAAAGATCTGAGAAAGCTGTATATTACACTTTGTGCGAGGTAGTCTTGCTGTATTTGGGG	3193
Db	301	CAAAGATCTGAGAAAGCTGTATATTACACTTTGTGCGAGGTAGTCTTGCTGTATTTGGGG	360
Qy	3194	AATTGCAAAGAAAGTGGAGCTGACAGAAATAACCCTTTTACAGTTTGTGCACTGTGTAC	3253
Db	361	AATTGCAAAGAAAGTGGAGCTGACAGAAATAACCCTTTTACAGTTTGTGCACTGTGTAC	420
Qy	3254	GGTCTGTGTAGGTTGATGCAGATTTTCTGAAATGAAATGTTTAGACGAGATCATGCCACC	3313
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Qy 3314 AAGGCAGGAGTGAAAAAGCTTGCCTTTCCTGGTATGTTCTAGGTGTATTGTGAAATTTAC 3373
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 Db 481 AAGGCAGGAGTGAAAAAGCTTGCCTTTCCTGGTATGTTCTAGGTGTATTGTGAAATTTAC 540
 Qy 3374 TGTGTATTAAATTGCCAATATAAGTAAATATAGAT--TATATATATCTATATATAGTGTT 3431
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 Db 601 TCACGAAGCTTAGCCCTTTACCTTCCCAGCT 631

RESULT 15

CB521332

LOCUS CB521332 822 bp mRNA linear EST 09-JUL-2003

DEFINITION UI-M-GH0-cem-h-13-0-UI.r1 NIH_BMAP_GH0 Mus musculus cDNA clone
 IMAGE:6841502 5', mRNA sequence.

ACCESSION CB521332

VERSION CB521332.1 GI:29354687

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 822)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Jim Lin, University of Iowa

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Distribution information can be found at

<http://genome.uiowa.edu/distribution/mousefl.html>

This clone was contributed by the Brain Molecular Anatomy Project
 (BMAP)

Seq primer: pYX-5.

FEATURES

source

Location/Qualifiers

1. .822

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6"

/db_xref="taxon:10090"

/clone="IMAGE:6841502"

/tissue_type="Whole brain"

/dev_stage="1, 5, and 15 days newborn"

/lab_host="DH10B (T1 phage resistant)"

/clone_lib="NIH_BMAP_GH0"

/note="Organ: Brain; Vector: pYX- Asc; Site_1: EcoR I;

Site_2: Not I; The library was constructed according

Bonaldo, Lennon and Soares, Genome Research, 6:791-806,

1996. Denatured RNA was size fractionated on a 1% agarose
 gel. First strand cDNA synthesis was primed with oligo-dT


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Qy      2545 AGGAGTTGGTTCAGAAGTACAGCAATTCTGCTCTTGGTCATGTTAACTGCACAATAAAAAG 2604
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Db      647 AGGAATTGGTTCAGAAATATAGTAATTCTGCTCTTGGTCATGTGAACAGCACAATAAAAAG 706
Qy      2605 AACTCAGACGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTGA 2664
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Db      707 AATTGAGGCGTCTCTTCTTAGTTGATGACTTAGTTGATTCCCTGAAGTTTGCAGTGTTGA 766
Qy      2665 TGTGGGTATTTACCTATGTTGGTGCCTTGTTCAATGGTCTGACACTACTAATTTT 2719
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Db      767 TGTGGGTATTTACTTACGTGGTGCCTTGTTCAATGGTTTGACACTACTGACTTT 821

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Search completed: September 11, 2004, 15:09:51
Job time : 9102.67 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 11, 2004, 00:39:35 ; Search time 14422.6 Seconds
(without alignments)
11519.006 Million cell updates/sec

Title: US-09-830-972-28
Perfect score: 3833
Sequence: 1 ctatctcctctctcagccgc.....ttaaaaaaaaaaaaaaaaaaaaa 3833

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
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6: gb_pat:*
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16: em_fun:*
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 39: em_htgo_hum:*
 40: em_htgo_mus:*
 41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	3	2716	70.9	4102	9	AY123245	AY123245 Homo sapi	
	4	2716	70.9	4109	9	AY123248	AY123248 Homo sapi	
	5	2716	70.9	4123	9	AY123247	AY123247 Homo sapi	
	6	2716	70.9	4160	9	AY123246	AY123246 Homo sapi	
	7	2716	70.9	4789	9	AY102279	AY102279 Homo sapi	
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	9	2649.8	69.1	4632	9	AF148537	AF148537 Homo sapi	
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	20	2167.2	56.5	4518	10	BC056373	BC056373 Mus muscu	
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c	32	1698	44.3	162692	2	AC016171	AC016171 Homo sapi	
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34	1414.6	36.9	1980	6	BD083733	BD083733 Nucleic a
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36	1378	36.0	60615	10	AY102286	AY102286 Mus muscu
37	1378	36.0	166516	2	AC135510	AC135510 Mus muscu
38	1378	36.0	211357	2	AC113284	AC113284 Mus muscu
39	1378	36.0	212042	10	AL929371	AL929371 Mouse DNA
c 40	1364.2	35.6	218532	2	AC131431	AC131431 Rattus no
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44	1033.4	27.0	1700	9	AF177332	AF177332 Homo sapi
45	1031.6	26.9	2276	9	AF132047	AF132047 Homo sapi

ALIGNMENTS

RESULT 1

AY123250

LOCUS AY123250 4060 bp mRNA linear PRI 23-SEP-2003

DEFINITION Homo sapiens RTN4 isoform G (RTN4) mRNA, complete cds; alternatively spliced.

ACCESSION AY123250

VERSION AY123250.1 GI:26800589

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 4060)

AUTHORS Oertle,T., Huber,C., van der Putten,H. and Schwab,M.E.

TITLE Genomic structure and functional characterisation of the promoters of human and mouse nogo/rtn4

JOURNAL J. Mol. Biol. 325 (2), 299-323 (2003)

MEDLINE 22376540

PUBMED 12488097

REFERENCE 2 (bases 1 to 4060)

AUTHORS Van der Putten,H.

TITLE Direct Submission

JOURNAL Submitted (07-MAY-2002) Nervous System Research, Novartis Pharma Inc., Basel, Switzerland

REFERENCE 3 (bases 1 to 4060)

AUTHORS Oertle,T. and Schwab,M.E.

TITLE Direct Submission

JOURNAL Submitted (17-MAY-2002) Brain Research Institute, University of Zurich and ETH Zurich, Winterthurerstr.190, Zuerich 8057, Switzerland

FEATURES

Location/Qualifiers

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gene 1. .4060

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ORIGIN

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Matches 3332;  Conservative  0;  Mismatches 445;  Indels  99;  Gaps  25;

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Db	1061	AACCCCTTTCCTTGTAGCAGCACAGGATTCTGAGACAGATTATGTCACAACAGATAATTTA	1120
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RESULT 3

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LOCUS AY123245 4102 bp mRNA linear PRI 23-SEP-2003

DEFINITION Homo sapiens RTN4 isoform Aa (RTN4) mRNA, complete cds;
 alternatively spliced.

ACCESSION AY123245

VERSION AY123245.1 GI:26800574

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 4102)

AUTHORS Oertle,T., Huber,C., van der Putten,H. and Schwab,M.E.

TITLE Genomic structure and functional characterisation of the promoters
 of human and mouse nogo/rtn4

JOURNAL J. Mol. Biol. 325 (2), 299-323 (2003)

MEDLINE 22376540

PUBMED 12488097

REFERENCE 2 (bases 1 to 4102)

AUTHORS Van der Putten,H.

TITLE Direct Submission

JOURNAL Submitted (07-MAY-2002) Nervous System Research, Novartis Pharma
 Inc., Basel, Switzerland

REFERENCE 3 (bases 1 to 4102)

AUTHORS Oertle,T. and Schwab,M.E.

TITLE Direct Submission

JOURNAL Submitted (17-MAY-2002) Brain Research Institute, University of
 Zurich and ETH Zurich, Winterthurerstr.190, Zuerich 8057,
 Switzerland

FEATURES Location/Qualifiers

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Db 1103 AACCCCTTTCCTTGTAGCAGCACAGGATTCTGAGACAGATTATGTCAACAGATAATTTA 1162

Qy 897 TCAAAGGTGACCGAGGAAGTAGTGGCAAACATGCCTGAAGGTCTAACCCCAGATTTGGTT 956
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Db 1163 ACAAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCCAGATTTAGTA 1222

Qy 957 CAGGAAGCATGTGAAAGTGAATTGAATGAAGCTACTGGTACAAAAAATTGCCTTTGAAACA 1016
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Qy 1017 AAAATGGACCTGGTTCAAACCTCAGAAGCTGTGCAGGAGTCACTTTACCCTGTAACACAG 1076
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Qy 1077 CTTTGCCCATCTTTTGAAGAATCTGAAGCTACTCCGTCACCGGTTTTGCCTGACATTGTC 1136
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Qy 1137 ATGGAAGCACCATTAAATTCTGTAGTTCCTAGTGCTGGTGCTTCTGCAGTGCAGCTCAGT 1196
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Qy 1197 TCATCACCATTAGAACTCTTCCTTCAGTTAATTATGAAAGCATAAAGTTTTGAGCCTGAA 1256
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 Db 2237 GTATCCACAAAAGTGAAATTGCTAATGCCCGGATGGAGCTGGGTTCATTGCCTTGACA 2296

Qy 2037 GGATTGCCCCATGACCTTTCTTTCAAGAGTATACAACC-----TAAAGAGGAAGTTCAT 2090
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Qy 2151 GATGTTTCTGCTTTGGATGCTCAAGCAGAGATAGGCAGCATAGAAAACCCAAAGTTCTT 2210

Db	2417									2476
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Db	2477	GTGAAAGAAGCTGAGAAAAA	ACTTCCTTCCGATACAGAAA	AAGAGGACAGATCACCATCT						2536
Qy	2271	GCTATATTTTCAGCAGAGCT	GAGTAAACTTCAGTTGTTG	ACCTCCTCTACTGGAGAGAC						2330
Db	2537	GCTATATTTTCAGCAGAGCT	GAGTAAACTTCAGTTGTTG	ACCTCCTGTACTGGAGAGAC						2596
Qy	2331	ATTAAGAAGACTGGAGTGGT	GTTTGGTGCCAGCTTGTTCC	TGCTGCTCTCGCTGACAGTA						2390
Db	2597	ATTAAGAAGACTGGAGTGGT	GTTTGGTGCCAGCCTATTCC	TGCTGCTTTTCATTGACAGTA						2656
Qy	2391	TTCAGCATTGTGAGTGTAAC	GGCCTACATTGCCTTGGCCCT	GCTCTCTGTGACTATCAGC						2450
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Qy	2451	TTTAGGATATATAAGGGTGT	GATCCAGGCTATCCAGAAATCT	GATGAAGGCCACCCATTC						2510
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Qy	2571	TCTGCTCTTGGTCATGTTAA	CTGCACAATAAAAGAACTCAG	ACGCCTCTTCTTAGTTGAT						2630
Db	2837	TCTGCTCTTGGTCATGTGA	ACTGCACGATAAAGGAACTCAG	GCCTCTTCTTAGTTGAT						2896
Qy	2631	GATTTAGTTGATTCTCTGA	AGTTTGCAGTGTTGATGTGGG	TATTTACCTATGTTGGTGCC						2690
Db	2897	GATTTAGTTGATTCTCTGA	AGTTTGCAGTGTTGATGTGGG	TATTTACCTATGTTGGTGCC						2956
Qy	2691	TTGTTCAATGGTCTGACACT	ACTAATTTTGGCTCTGATTT	CACTCTTCAGTGTTCCTGTT						2750
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Db	3137	AAACGCCCAAATAATTA----	GTAGGAGTTCATCTTTAAAG	GGGATATTCATTTGATT						3191
Qy	2931	CCATTGGGGAGGGTCAGGG	AAGAACAAGCCTTGACATTGC	AGTGCAGTTTCAC-----						2984
Db	3192	ATACGGGGAGGGTCAGGG	AAGAACGAA-CCTTGACGTTGC	AGTGCAGTTTCACAGATCG						3250
Qy	2985	-----AGATCTTTATTTT	TAGCAACGCAGTG-TCTGAGG	AAAAATGACCTGTCTTGACTG						3038

Db	3251	TTGTTAGATCTTTATTTTTAGCCATGCACCTGTTGTGAGGAAAAATTACCTGTCTTGACTG	3310
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Db	3311	CCATGTGTTTCATCATCTTAAGTATTGTAAGCTGCTATGTATGGATTTAAACCGTAATCAT	3370
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Db	3371	A--TCTTTTTCCTATCTGAGGCACTGGTGA-----ATAAAAAACCTGTATATT	3417
QY	3159	ACACTTTGTGCGAGGTAGTCTTGCTGTAT--TTGGGGAATTGCAAAGAAAGTGGAGCT---	3214
Db	3418	TTACTTTGTGTCAGATAGTCTTGCCGCATCTTGGCAAGTTGCAGAGATGGTGGAGCTAGA	3477
QY	3215	---GACAGAAATAACCCTTTTACAGTTTGTGCACTGTGTACGGTCTGTGTAGGTTGATG	3271
Db	3478	AAAAAAAAAAAAAAGCCCTTTTCAGTTTGTGCACTGTGTATGGTCCGTGTAGATTGATG	3537
QY	3272	CAGATTTTCTGAAATGAAA----TGTTTAGACGAGATCATGCCACCAAGGCAGGAGTGAA	3327
Db	3538	CAGATTTTCTGAAATGAAATGTTTGTTTAGACGAGATCATACCGGTAAAGCAGGAATGAC	3597
QY	3328	AAAGCTTGCCTTTCTGGTATGTTCTAGGTGTATTGTGAAATTTACTGTTGTATTAATTG	3387
Db	3598	AAAGCTTG-CTTTTCTGGTATGTTCTAGGTGTATTGTGACTTTTACTGTTATATTAATTG	3656
QY	3388	CCAATATAAGTAAATATAGATTATATATATCTATATATAGTGTTTCACGAAGCTTAGCCC	3447
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QY	3448	TTTACCTTCCCAGCTGCCCCACAGTGCTTGATACT-----TCTGTCATGGGTTTTATGT	3501
Db	3711	TTTACCTT-CCAGCCACCCACAGTGCTTGATATTTTACAGAGTCAGTCATTGGTTATACAT	3769
QY	3502	GTGTAGTCCCAAAGCACATAAGCTAGGGAGAAACGTACTTCTAGGCGCACTACCATCTGT	3561
Db	3770	GTGTAGTTCCCAAAGCACATAAGCTAGAAGAAGAAATATTTCTAGGAGCACTACCATCTGT	3829
QY	3562	TTTCAACACGAACCGACGCCATGCAAACAGAACTCC-TCAACATAAACTTCACTGCACAG	3620
Db	3830	TTTCAACATGAA---ATGCCACACACATAGAAGCTCCAACAACATCAATTTTCATTGCACAG	3886
QY	3621	ACTTACTGTAGTTAATTTTATCAC--AAACTCTGGACTGAATCTAATGCTTCCAAAAA--	3676
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QY	3677	-----TGTTTGCAAATATCAAACATTGTTATGTAAGAAAATAT-----AAATGACGA	3723
Db	3947	TTGTTTGTTTGCAAATATCAAACATTGTTATGCAAGAAATTATTAATTACAAAATGAAGA	4006
QY	3724	TTTATACAATTGTGGTTTAAGCTGTATTGAACTAAATCTGTGGAATGCATTGTGAACTGT	3783
Db	4007	TTTATACCATTGTGGTTTAAGCTGTACTGAACTAAATCTGTGGAATGCATTGTGAACTGT	4066
QY	3784	AAAAGCAAAGTATCAATAAAGCTTATAGACTTAAAA	3819
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RESULT 4

AY123248

LOCUS AY123248 4109 bp mRNA linear PRI 23-SEP-2003

DEFINITION Homo sapiens RTN4 isoform E (RTN4) mRNA, complete cds;
alternatively spliced.

ACCESSION AY123248

VERSION AY123248.1 GI:26800583

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 4109)

AUTHORS Oertle,T., Huber,C., van der Putten,H. and Schwab,M.E.

TITLE Genomic structure and functional characterisation of the promoters
of human and mouse nogo/rtn4

JOURNAL J. Mol. Biol. 325 (2), 299-323 (2003)

MEDLINE 22376540

PUBMED 12488097

REFERENCE 2 (bases 1 to 4109)

AUTHORS Van der Putten,H.

TITLE Direct Submission

JOURNAL Submitted (07-MAY-2002) Nervous System Research, Novartis Pharma
Inc., Basel, Switzerland

REFERENCE 3 (bases 1 to 4109)

AUTHORS Oertle,T. and Schwab,M.E.

TITLE Direct Submission

JOURNAL Submitted (17-MAY-2002) Brain Research Institute, University of
Zurich and ETH Zurich, Winterthurerstr.190, Zuerich 8057,
Switzerland

FEATURES Location/Qualifiers

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183. .3143

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ORIGIN

Query Match 70.9%; Score 2716; DB 9; Length 4109;
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Qy	481	AAAGATACTTACAAGCAAGATAGTGATGTTTTGATTGCTGGAGGTAATATAGAGAGCAAA	540
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Qy	541	TTGGAAGGTAAAGTGGATAAGAAACACTTTTCAGATAGCCTTGAACAAACAAATCGTGAA	600
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Qy	957	CAGGAAGCATGTGAAAGTGAATTGAATGAAGCTACTGGTACAAAATTGCCTTTGAAACA	1016
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Db	1410	ATGGAAGCACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGATACAGCCCAGC	1469
Qy	1197	TCATCACCATTAGAACTCTTCCTTCAGTTAATTATGAAAGCATAAAGTTTGAGCCTGAA	1256
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Qy	1317	GAAGAAATCACAGAGCCTGAAGGTATTAGTGTAGCTGTTTCAGGAAACAGAAGCTCCTTAT	1376
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Db	1707	 TTCTCTGATTATTCAGAAATGGCAAAGTTGAACAGCCAGTGCCTGATCATTCTGAGCTA	1766
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Db	1944	 GAGGGAGGAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATACC	2003
Qy	1737	TTAGCACCTGATGAAGTTTCAGCATTGACCCAAAAGGAGAAAATCCCTTTGCAGATGGAG	1796
Db	2004	 CTGTTACCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAATTCCTTTGCAGATGGAG	2063
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Db	2064	 GAGCTCAGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGATA	2123
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Db	2124	 AGAGAAACTGAAACGTTTTCAGATTTCATCTCCAATTGAAATTATAGATGAGTTCCCTACA	2183
Qy	1917	TTTGTCAGTTCTAAAGCAGATTCTTCTCCTACATTAGCCAGGGAATACACTGACCTAGAA	1976
Db	2184	 TTGATCAGTTCTAAAACTGATTCAATTTCTAAATTAGCCAGGGAATATACTGACCTAGAA	2243
Qy	1977	GTAGCCACAAAAGTGAAATTGCTGACATCCAGGATGGAGCTGGGTCATTGGCTTGTGCA	2036
Db	2244	 GTATCCACAAAAGTGAAATTGCTAATGCCCCGGATGGAGCTGGGTCATTGCCTTGCACA	2303
Qy	2037	GGATTGCCCCATGACCTTTCTTTCAAGAGTATACAACC-----TAAAGAGGAAGTTCAT	2090
Db	2304	 GAATTGCCCCATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCAGT	2363
Qy	2091	GTCCCAGATGAGTTCTCCAAAGATAGGGGTGATGTTTCAAAGGTGCCCGTACTGCCTCCA	2150
Db	2364	 TTCTCAGATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCA	2423
Qy	2151	GATGTTTCTGCTTTGGATGCTCAAGCAGAGATAGGCAGCATAGAAAAACCCAAAGTTCTT	2210
Db	2424	 GATGTTTCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTT	2483
Qy	2211	GTGAAAGAAGCCGAGAGAAAACCTTCCTTCTGATACAGAAAAAGAGCGAAGATCTCCATCT	2270

Db	2484	GTGAAAGAAGCTGAGAAAAAACTTCCTTCCGATACAGAAAAAGAGGACAGATCACCATCT	2543
Qy	2271	GCTATATTTTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGAC	2330
Db	2544	GCTATATTTTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTGTACTGGAGAGAC	2603
Qy	2331	ATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCTTGTTCCCTGCTGCTCTCGCTGACAGTA	2390
Db	2604	ATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCCTATTCCTGCTGCTTTTCATTGACAGTA	2663
Qy	2391	TTCAGCATTGTGAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCTGTGACTATCAGC	2450
Db	2664	TTCAGCATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGC	2723
Qy	2451	TTTAGGATATATAAGGGTGTGATCCAGGCTATCCAGAAATCTGATGAAGGCCACCCATTC	2510
Db	2724	TTTAGGATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTC	2783
Qy	2511	AGGGCATATTTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGCAAT	2570
Db	2784	AGGGCATATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGTAAT	2843
Qy	2571	TCTGCTCTTGGTCATGTAACTGCACAATAAAAGAACTCAGACGCCTCTTCTTAGTTGAT	2630
Db	2844	TCTGCTCTTGGTCATGTGAACTGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGAT	2903
Qy	2631	GATTTAGTTGATTCTCTGAAGTTTGCACTGTTGATGTGGGTATTTACCTATGTTGGTGCC	2690
Db	2904	GATTTAGTTGATTCTCTGAAGTTTGCACTGTTGATGTGGGTATTTACCTATGTTGGTGCC	2963
Qy	2691	TTGTTCAATGGTCTGACACTACTAATTTTGGCTCTGATTTCACTCTTCAGTGTTCCCTGTT	2750
Db	2964	TTGTTTAATGGTCTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTTCCCTGTT	3023
Qy	2751	ATTTATGAACGGCATCAGGCGCAAATAGATCATTATCTGGGACTTGCAAATAAGAATGTT	2810
Db	3024	ATTTATGAACGGCATCAGGCACAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTT	3083
Qy	2811	AAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGAATGA	2870
Db	3084	AAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGAATGA	3143
Qy	2871	GAAAGCCTGAAAGAGTTAACAATAGAGGAGTTTATCTTTAAAGGGGATATTCATTTGATT	2930
Db	3144	AAACGCCCAAATAATTA-----GTAGGAGTTCATCTTTAAAGGGGATATTCATTTGATT	3198
Qy	2931	CCATTGGGGAGGGTCAGGGAAGAACAAGCCTTGACATTGCAGTGCAGTTTCAC-----	2984
Db	3199	ATACGGGGGAGGGTCAGGGAAGAACGAA-CCTTGACGTTGCAGTGCAGTTTCACAGATCG	3257
Qy	2985	-----AGATCTTTATTTTGTAGCAACGCAGTG-TCTGAGGAAAAATGACCTGTCTTGACTG	3038
Db	3258	TTGTTAGATCTTTATTTTGTAGCCATGCACTGTTGTGAGGAAAAATTACCTGTCTTGACTG	3317
Qy	3039	CCCTGTGTTTCATCATCTTAAGTATTGTAAGCTGCTATGTATGGATTTAAATCGTAATCAT	3098
Db	3318	CCATGTGTTTCATCATCTTAAGTATTGTAAGCTGCTATGTATGGATTTAAACCGTAATCAT	3377

DEFINITION Homo sapiens RTN4 isoform D (RTN4) mRNA, complete cds;
 alternatively spliced.

ACCESSION AY123247

VERSION AY123247.1 GI:26800580

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 4123)

AUTHORS Oertle,T., Huber,C., van der Putten,H. and Schwab,M.E.

TITLE Genomic structure and functional characterisation of the promoters
 of human and mouse nogo/rtn4

JOURNAL J. Mol. Biol. 325 (2), 299-323 (2003)

MEDLINE 22376540

PUBMED 12488097

REFERENCE 2 (bases 1 to 4123)

AUTHORS Van der Putten,H.

TITLE Direct Submission

JOURNAL Submitted (07-MAY-2002) Nervous System Research, Novartis Pharma
 Inc., Basel, Switzerland

REFERENCE 3 (bases 1 to 4123)

AUTHORS Oertle,T. and Schwab,M.E.

TITLE Direct Submission

JOURNAL Submitted (17-MAY-2002) Brain Research Institute, University of
 Zurich and ETH Zurich, Winterthurerstr.190, Zuerich 8057,
 Switzerland

FEATURES

source	Location/Qualifiers 1. .4123 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /chromosome="2" /map="2p16" /tissue_type="testis"
gene	1. .4123 /gene="RTN4" /note="synonym: NOGO"
5'UTR	1. .196 /gene="RTN4"
CDS	197. .3157 /gene="RTN4" /note="RTN4-D; alternatively spliced" /codon_start=1 /product="RTN4 isoform D" /protein_id="AAM64251.1" /db_xref="GI:26800581" /translation="MDLKEQPGNTISAGQEDFPSVLLETAASLPSLSPLSAASFKEHE YLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEMGSFSVSP KAESAVIVANPREEIIIVKNKDEEEKLVSNILHNQQELPTALTCLKVEDEVVSSEKAK DSFNEKRVAVEAPMREEYADFKPFERWVEVKDSKEDSDMLAAGGKIESNLESKVDDKKC FADSLEQTNHEKDSSESNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIFPL LGDPTSENKTDEKKIEEKKAQIVTEKNTSTKTSNPFLVAAQDSETDYVTDLNLTKVTE EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCP SFESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENP PPYEEAMSVSLKKVSGIKKEIKPENINAALQETEAPYISACDLIKETKLSAEPAPD FSDYSEMAKVEQPVPDHSSELVEDSSPDSEPVDLFSDDSI DPVPQKQDETVMVKESLT

ETSFESMIEYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPL
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 KVLLLLPPDV SALATQAEIESIVKPKVLVKEAEKKLP SDEKEDRSPSAIFSAELSKTS
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 AIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLK
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3'UTR

ORIGIN

Query Match 70.9%; Score 2716; DB 9; Length 4123;
 Best Local Similarity 86.0%; Pred. No. 0;
 Matches 3332; Conservative 0; Mismatches 445; Indels 99; Gaps 25;

Qy	1	CTATCTCCTCTCTCAGCCGCTGCTTTTAAAGAACGTGAATACCTTGGTGATTTACCAGCA	60
Db	290	CTGTCTCCTCTCTCAGCCGCTTCTTCAAAGAACATGAATACCTTGGTAATTTGTCAACA	349
Qy	61	GTA CTGCCC ACTGAAGGAACACTTCCAGCAACTTCAAATGAAGCTTCTAAAGCATTCTCA	120
Db	350	GTATTACCCACTGAAGGAACACTTCAAGAAAATGTCAGTGAAGCTTCTAAAGAGGTCTCA	409
Qy	121	GAGAAGGC AAAAAATCCATTTGTAGAGAGAAATTTAACAGAATTTTCAGAATTGGAATAT	180
Db	410	GAGAAGGC AAAAACTCTACTCATAGATAGAGATTTAACAGAGTTTTCAGAATTAGAATAC	469
Qy	181	TCAGAAATGGAATCATCATT CAGTGGCTCTCAAAAGGCAGAACCTGCCGTAACAGTAGCG	240
Db	470	TCAGAAATGGGATCATCGTT CAGTGTCTCTCCAAAAGCAGAACTGCGGTAATAGTAGCA	529
Qy	241	AATCCTAGGGACGAAATAGTTGTGAGGAGTAGAGATAAAGAAGAGGACTTAGTTAGTCTT	300
Db	530	AATCCTAGGGAAGAAATAATCGTGAAAAATAAAGATGAAGAAGAGAAGTTAGTTAGTAAT	589
Qy	301	AACATCCTTCATACTCAGCAGGAGTTATCTACAGTCCCTTACGAAATCAGTTGAAGAAGAA	360
Db	590	AACATCCTTCATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTTGGTTAAAGAGGAT	649
Qy	361	GATAGAGTTCTGTCTCCAGAAAAACAAAGGACAGTTTAAAGGAAAAGGGAGTTGCAGCA	420
Db	650	GA---AGTTGTGTCTTCAGAAAAAGCAAAAGACAGTTTAAATGAAAAGAGAGTTGCAGTG	706
Qy	421	GAAGCTTCTATGGGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTG	480
Db	707	GAAGCTCCTATGAGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTG	766
Qy	481	AAAGATACTTACAAGCAAGATAGTGATGTTTTGATTGCTGGAGGTAATATAGAGAGCAAA	540
Db	767	AAAGATAGT---AAGGAAGATAGTGATATGTTGGCTGCTGGAGGTAAATCGAGAGCAAC	823
Qy	541	TTGGAAGGTAAAGTGGATAAGAAACACTTTTTCAGATAGCCTTGAACAAACAAATCGTGAA	600
Db	824	TTGGAAGGTAAAGTGGATAAAAAATGTTTTGCAGATAGCCTTGAACAAACTAATCACGAA	883
Qy	601	AAAGATAGTGAAAGCAGTAATGATGACACTTCATTTCCAGTACACCAGAAGCTGTAAGA	660

Db	884	 AAAGATAGTGAGAGTAGTAATGATGATACTTCTTTCCCCAGTACGCCAGAAGGTATAAAG	943
Qy	661	GGTGGTTCCGGAGCGTACATCACGTGTGCTCCCTTTAACC---CAACAACCTGAGAATGTT	717
Db	944	 GATCGTTCAGGAGCATATATCACATGTGCTCCCTTTAACCCAGCAGCAACTGAGAGCATT	1003
Qy	718	TCAACAAACATTTTTCCCTTGTTGGAAGATCATACTTCGGAAAATAAGACAGATGAAAAA	777
Db	1004	 GCAACAAACATTTTTCCCTTGTTAGGAGATCCTACTTCAGAAAATAAGACCGATGAAAAA	1063
Qy	778	AAGATAGAA-AAAAAAGGCACAAATTGTAACAGAGAAGAATGCAAGTGTCAAGACATCA	836
Db	1064	 AAAATAGAAGAAAAGAAGGCCAAATAGTAACAGAGAAGAATACTAGCACCAAACATCA	1123
Qy	837	AACCCCTTTCCTTATGGCAGCACAGGAGTCTAAGACAGATTACGTTACAACAGATCATGTG	896
Db	1124	 AACCCCTTTCCTTGTAGCAGCACAGGATTCTGAGACAGATTATGTCACAACAGATAATTTA	1183
Qy	897	TCAAAGGTGACCGAGGAAGTAGTGGCAAACATGCCTGAAGGTCTAACCCAGATTTGGTT	956
Db	1184	 ACAAAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCCAGATTTAGTA	1243
Qy	957	CAGGAAGCATGTGAAAGTGAATTGAATGAAGCTACTGGTACAAAAATTGCCTTTGAAACA	1016
Db	1244	 CAGGAAGCATGTGAAAGTGAATTGAATGAAGTTACTGGTACAAAGATTGCTTATGAAACA	1303
Qy	1017	AAAATGGACCTGGTTCAAACCTCAGAAGCTGTGCAGGAGTCACTTTACCCTGTAACACAG	1076
Db	1304	 AAAATGGACTTGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCACAG	1363
Qy	1077	CTTTGCCCATCTTTTGAAGAATCTGAAGCTACTCCGTCACCGGTTTTGCCTGACATTGTC	1136
Db	1364	 CTTTGCCCATCATTTGAAGAGTCAGAAGCTACTCCTTCACCAGTTTTGCCTGACATTGTT	1423
Qy	1137	ATGGAAGCACCATTAAATTCTGTAGTTCCTAGTGCTGGTGCTTCTGCAGTGCAGCTCAGT	1196
Db	1424	 ATGGAAGCACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTCATACAGCCCAGC	1483
Qy	1197	TCATCACCATTAGAACTCTTCCTTCAGTTAATTATGAAAGCATAAAGTTTGAGCCTGAA	1256
Db	1484	 TCATCACCATTAGAAGC---TTCTTCAGTTAATTATGAAAGCATAAAACATGAGCCTGAA	1540
Qy	1257	AATCCCCCACCATATGAGGAGGCCATGAATGTATCACTAAAAAAGAATCAGGAATGAAT	1316
Db	1541	 AATCCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAGTATCAGGAATAAAG	1600
Qy	1317	GAAGAAATCACAGAGCCTGAAGGTATTAGTGTAGCTGTTGAGGAAACAGAAGCTCCTTAT	1376
Db	1601	 GAAGAAATTAAAGAGCCTGAAAATATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTAT	1660
Qy	1377	ATATCTATTGCATGTGATTTAATTAAAGAAACAAAGATCTCTACTGAACCGACTCCAGAT	1436
Db	1661	 ATATCTATTGCATGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAACCGACTCCGGAT	1720
Qy	1437	TTCTCTAGTTATTTCAGAAATAGCAGAAGTTGCACAGCCAGTGCCCGAGCATTCTGAGCTA	1496

Db	1721	TTCTCTGATTATTTCAGAAATGGCAAAAGTTGAACAGCCAGTGCCTGATCATTCTGAGCTA	1780
Qy	1497	GTTGAAGATTCCCTCCCCCGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCC	1556
Db	1781	GTTGAAGATTCCCTCACCTGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCT	1840
Qy	1557	GAAGTTCCACAAAAACAAGATGAAGCTGTAATACTTGTGAAAGAAAACCTCACTGAAATT	1616
Db	1841	GACGTTCCACAAAAACAAGATGAAACTGTGATGCTTGTGAAAGAAAGTCTCACTGAGACT	1900
Qy	1617	TCATCTGAGTCAATGACAGGACATGACAATAAGGGAAAACTCAGTGCTTCACCATCACCT	1676
Db	1901	TCATTTGAGTCAATGATAGAATATGAAAAATAAGGAAAAAACTCAGTGCTTTGC---CACCT	1957
Qy	1677	GAGGGAGGAAAAACCGTATTTGGAGTCTTTTCAGCCCAGTTTAGGCATCACAAAAGATACC	1736
Db	1958	GAGGGAGGAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATACC	2017
Qy	1737	TTAGCACCTGATGAAGTTTCAGCATTGACCCAAAAGGAGAAAATCCCTTTGCAGATGGAG	1796
Db	2018	CTGTTACCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAATTCCTTTGCAGATGGAG	2077
Qy	1797	GAGCTCAATACTGCAGTTTATTCAAGTGATGGCTTATTCATTGCTCAGGAAGCAAACCTA	1856
Db	2078	GAGCTCAGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGATA	2137
Qy	1857	AGAGAAAGTGAAACATTTTCAGATTCATCTCCGATTGAGATTATAGATGAGTTCCCGACC	1916
Db	2138	AGAGAAACTGAAACGTTTTCAGATTCATCTCCAATTGAAATTATAGATGAGTTCCCTACA	2197
Qy	1917	TTTGTGAGTTCTAAAGCAGATTCTTCTCCTACATTAGCCAGGGAATACACTGACCTAGAA	1976
Db	2198	TTGATCAGTTCTAAAACTGATTCAATTTCTAAATTAGCCAGGGAATATACTGACCTAGAA	2257
Qy	1977	GTAGCCACAAAAAGTGAAATTGCTGACATCCAGGATGGAGCTGGGTTCATTGGCTTGTGCA	2036
Db	2258	GTATCCACAAAAAGTGAAATTGCTAATGCCCCGGATGGAGCTGGGTTCATTGCCTTGCACA	2317
Qy	2037	GGATTGCCCCATGACCTTTCTTTCAAGAGTATACAACC-----TAAAGAGGAAGTTCAT	2090
Db	2318	GAATTGCCCCATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCAGT	2377
Qy	2091	GTCCCAGATGAGTTCTCCAAAGATAGGGGTGATGTTTCAAAGGTGCCCCGACTGCCTCCA	2150
Db	2378	TTCTCAGATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCA	2437
Qy	2151	GATGTTTCTGCTTTGGATGCTCAAGCAGAGATAGGCAGCATAGAAAAACCCAAAGTTCTT	2210
Db	2438	GATGTTTCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTT	2497
Qy	2211	GTGAAAGAAGCCGAGAGAAAACTTCCTTCTGATACAGAAAAAGAGCGAAGATCTCCATCT	2270
Db	2498	GTGAAAGAAGCTGAGAAAAAACTTCCTTCCGATACAGAAAAAGAGGACAGATCACCATCT	2557
Qy	2271	GCTATATTTTTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGAC	2330
Db	2558	GCTATATTTTTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTGTACTGGAGAGAC	2617

Qy	2331	ATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCTTGTTCCCTGCTGCTCTCGCTGACAGTA	2390
Db	2618	ATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCCTATTCCCTGCTGCTTTTCATTGACAGTA	2677
Qy	2391	TTCAGCATTGTGAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCTGTGACTATCAGC	2450
Db	2678	TTCAGCATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGC	2737
Qy	2451	TTTAGGATATATAAGGGTGTGATCCAGGCTATCCAGAAATCTGATGAAGGCCACCCATTC	2510
Db	2738	TTTAGGATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTC	2797
Qy	2511	AGGGCATATTTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGCAAT	2570
Db	2798	AGGGCATATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGTAAT	2857
Qy	2571	TCTGCTCTTGGTCATGTAACTGCACAATAAAAGAACTCAGACGCCTCTTCTTAGTTGAT	2630
Db	2858	TCTGCTCTTGGTCATGTGAAGTGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGAT	2917
Qy	2631	GATTTAGTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCC	2690
Db	2918	GATTTAGTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCC	2977
Qy	2691	TTGTTCAATGGTCTGACACTACTAATTTTGGCTCTGATTTCACTCTTCAGTGTTCCCTGTT	2750
Db	2978	TTGTTTAATGGTCTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTTCCCTGTT	3037
Qy	2751	ATTTATGAACGGCATCAGGCGCAAATAGATCATTATCTGGGACTTGCAAATAAGAATGTT	2810
Db	3038	ATTTATGAACGGCATCAGGCACAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTT	3097
Qy	2811	AAAGATGCTATGGCTAAAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGAATGA	2870
Db	3098	AAAGATGCTATGGCTAAAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGAATGA	3157
Qy	2871	GAAAGCCTGAAAGAGTTAACAATAGAGGAGTTTATCTTTAAAGGGGATATTCATTTGATT	2930
Db	3158	AAACGCCCAAATAATTA-----GTAGGAGTTCATCTTTAAAGGGGATATTCATTTGATT	3212
Qy	2931	CCATTGGGGAGGGTCAGGGAAGAACAAAGCCTTGACATTGCAGTGCAGTTTCAC-----	2984
Db	3213	ATACGGGGAGGGTCAGGGAAGAACGAA-CCTTGACGTTGCAGTGCAGTTTCACAGATCG	3271
Qy	2985	-----AGATCTTTATTTTGTAGCAACGCAGTG-TCTGAGGAAAAATGACCTGTCTTGACTG	3038
Db	3272	TTGTTAGATCTTTATTTTGTAGCCATGCACTGTTGTGAGGAAAAATTACCTGTCTTGACTG	3331
Qy	3039	CCCTGTGTTTCATCATCTTAAGTATTGTAAGCTGCTATGTATGGATTTAAATCGTAATCAT	3098
Db	3332	CCATGTGTTTCATCATCTTAAGTATTGTAAGCTGCTATGTATGGATTTAAACCGTAATCAT	3391
Qy	3099	ATTTGTTTTTCTGTATGAGGCACTGGTGAATAAACAAAGATCTGAGAAAGCTGTATATT	3158
Db	3392	A--TCTTTTTCTATCTGAGGCACTGGTGGA-----ATAAAAAACCTGTATATT	3438

Qy 3159 ACACTTTGTCGCAGGTAGTCTTGCTGTAT-TTGGGGAATTGCAAAGAAAGTGGAGCT--- 3214
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 Db 3439 TTACTTTGTTGCAGATAGTCTTGCCGCATCTTGGCAAGTTGCAGAGATGGTGGAGCTAGA 3498
 Qy 3215 ---GACAGAAATAACCCCTTTTCACAGTTTGTGCACTGTGTACGGTCTGTGTAGGTTGATG 3271
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 Db 3499 AAAAAAAAAAAAAAGCCCTTTTCAGTTTGTGCACTGTGTATGGTCCGTGTAGATTGATG 3558
 Qy 3272 CAGATTTTCTGAAATGAAA----TGTTTAGACGAGATCATGCCACCAAGGCAGGAGTGAA 3327
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 Db 3559 CAGATTTTCTGAAATGAAATGTTTGTTTAGACGAGATCATACCGGTAAAGCAGGAATGAC 3618
 Qy 3328 AAAGCTTGCCTTTCTGGTATGTTCTAGGTGTATTGTGAAATTTACTGTTGTATTAATTG 3387
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 Qy 3388 CCAATATAAGTAAATATAGATTATATATATCTATATATAGTGTTCACGAAGCTTAGCCC 3447
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 Db 3678 CCAATATAAGTAAATATAGATTATA-----TATGTATAGTGTTCACAAAGCTTAGACC 3731
 Qy 3448 TTTACCTTCCCAGCTGCCCCACAGTGCTTGATACT-----TCTGTCATGGGTTTTATGT 3501
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 Db 3732 TTTACCTT-CCAGCCACCCACAGTGCTTGATATTTTCTAGAGTCAGTCATTGGTTATACAT 3790
 Qy 3502 GTGTAGTCCCAAAGCACATAAGCTAGGGAGAAACGTACTTCTAGGCGCACTACCATCTGT 3561
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 Db 3791 GTGTAGTTCCCAAAGCACATAAGCTAGAAGAAGAAATATTTCTAGGAGCACTACCATCTGT 3850
 Qy 3562 TTTCAACACGAACCGACGCCATGCAAACAGAAGTCC-TCAACATAAACTTCACTGCACAG 3620
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 Db 3851 TTTCAACATGAA---ATGCCACACACATAGAAGTCCAACAACATCAATTTTCATTGCACAG 3907
 Qy 3621 ACTTACTGTAGTTAATTTTATCAC--AAACTCTGGACTGAATCTAATGCTTCCAAAAA-- 3676
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 Db 3908 ACTGACTGTAGTTAATTTTGTACAGAATCTATGGACTGAATCTAATGCTTCCAAAAATG 3967
 Qy 3677 -----TGTTTGCAAATATCAAACATTGTTATGTAAGAAAATAT-----AAATGACGA 3723
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 Db 3968 TTGTTTGTGTTTGCAAATATCAAACATTGTTATGCAAGAAATATTAATTACAAAATGAAGA 4027
 Qy 3724 TTTATACAATTGTGGTTTAAGCTGTATTGAACTAAATCTGTGGAATGCATTGTGAACTGT 3783
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 Db 4028 TTTATACCATTGTGGTTTAAGCTGTACTGAACTAAATCTGTGGAATGCATTGTGAACTGT 4087
 Qy 3784 AAAAGCAAAGTATCAATAAAGCTTATAGACTTAAAA 3819
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 Db 4088 AAAAGCAAAGTATCAATAAAGCTTATAGACTTAAAA 4123

RESULT 6

AY123246

LOCUS AY123246 4160 bp mRNA linear PRI 23-SEP-2003

DEFINITION Homo sapiens RTN4 isoform Ab (RTN4) mRNA, complete cds;
 alternatively spliced.

ACCESSION AY123246

VERSION AY123246.1 GI:26800577

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 4160)

AUTHORS Oertle,T., Huber,C., van der Putten,H. and Schwab,M.E.

TITLE Genomic structure and functional characterisation of the promoters
of human and mouse nogo/rtn4

JOURNAL J. Mol. Biol. 325 (2), 299-323 (2003)

MEDLINE 22376540

PUBMED 12488097

REFERENCE 2 (bases 1 to 4160)

AUTHORS Van der Putten,H.

TITLE Direct Submission

JOURNAL Submitted (07-MAY-2002) Nervous System Research, Novartis Pharma
Inc., Basel, Switzerland

REFERENCE 3 (bases 1 to 4160)

AUTHORS Oertle,T. and Schwab,M.E.

TITLE Direct Submission

JOURNAL Submitted (17-MAY-2002) Brain Research Institute, University of
Zurich and ETH Zurich, Winterthurerstr.190, Zuerich 8057,
Switzerland

FEATURES

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AUTHORS Oertle,T., Huber,C., van der Putten,H. and Schwab,M.E.
 TITLE Genomic structure and functional characterisation of the promoters
 of human and mouse nogo/rtn4
 JOURNAL J. Mol. Biol. 325 (2), 299-323 (2003)
 MEDLINE 22376540
 PUBMED 12488097
 REFERENCE 2 (bases 1 to 4789)
 AUTHORS Oertle,T. and Schwab,M.E.
 TITLE Direct Submission
 JOURNAL Submitted (07-MAY-2002) Brain Research Institute, University of
 Zurich and ETH Zurich, Winterthurerstr.190, Zuerich 8057,
 Switzerland
 REFERENCE 3 (bases 1 to 4789)
 AUTHORS Van der Putten,H.
 TITLE Direct Submission
 JOURNAL Submitted (07-MAY-2002) Nervous System Research, Novartis Pharma
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Db	2150	TCATCACCATTAGAAGC---TTCTTCAGTTAATTATGAAAGCATAAAACATGAGCCTGAA	2206
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Db	2267	GAAGAAATTAAAGAGCCTGAAAATATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTAT	2326
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Db	2327	ATATCTATTGCATGTGATTTAATTAAAGAAACAAAGCTTCTGCTGAACCAGCTCCGGAT	2386
Qy	1437	TTCTCTAGTTATTCAGAAATAGCAGAAGTTGCACAGCCAGTGCCCGAGCATTCTGAGCTA	1496
Db	2387	TTCTCTGATTATTCAGAAATGGCAAAAGTTGAACAGCCAGTGCCTGATCATTCTGAGCTA	2446
Qy	1497	GTTGAAGATTCCCTCCCCGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCC	1556
Db	2447	GTTGAAGATTCCCTCACCTGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCT	2506
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Qy	1917	TTTGTCAAGTTCTAAAGCAGATTCTTCTCCTACATTAGCCAGGGAATACACTGACCTAGAA	1976
Db	2864	TTGATCAGTTCTAAACTGATTTCATTTCTAAATTAGCCAGGGAATATACTGACCTAGAA	2923
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Db	2924	GTATCCACAAAAGTGAAATTGCTAATGCCCCGGATGGAGCTGGGTTCATTGCCTTGCACA	2983
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Db	2984	GAATTGCCCCATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCAGT	3043
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Db	3344	TTCAGCATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGC	3403
Qy	2451	TTTAGGATATATAAGGGTGTGATCCAGGCTATCCAGAAATCTGATGAAGGCCACCCATTC	2510
Db	3404	TTTAGGATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTC	3463
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Qy	2985	-----AGATCTTTATTTTGTAGCAACGCAGTG-TCTGAGGAAAAATGACCTGTCTTGACTG	3038
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Qy	3099	ATTTGTTTTTCTGTATGAGGCACTGGTGAATAAACAAAGATCTGAGAAAGCTGTATATT	3158
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Qy	3159	ACACTTTGTGCGCAGGTAGTCTTGCTGTAT-TTGGGGAATTGCAAAGAAAGTGGAGCT---	3214
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Qy	3215	---GACAGAAATAACCCCTTTTACAGTTTGTGCACTGTGTACGGTCTGTGTAGGTTGATG	3271
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Db    1381 GAAGCTCCTATGAGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTG 1440

Qy    481 AAAGATACTTACAAGCAAGATAGTGATGTTTTGATTGCTGGAGGTAATATAGAGAGCAAA 540
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Qy	895	TGTCAAAGGTGACCGAGGAAGTAGTGGCAAACATGCCTGAAGGTCTAACCCAGATTGG	954
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Qy	1135	TCATGGAAGCACCATTAAATTCTGTAGTTCCTAGTGCTGGTGCTTCTGCAGTGCAGCTCA	1194
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Qy	1855	TAAGAGAAAGTGAAACATTTTCAGATTTCATCTCCGATTGAGATTATAGATGAGTTCCCGA	1914
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Qy	1915	CCTTTGTGCTAGTTCTAAAGCAGATTCTTCTCCTACATTAGCCAGGGAATACACTGACCTAG	1974
Db	2872	CATTGATCAGTTCTAAAACTGATTCAATTTCTAAATTAGCCAGGGAATATACTGACCTAG	2931
Qy	1975	AAGTAGCCACAAAAAGTGAAATTGCTGACATCCAGGATGGAGCTGGGTCATTGGCTTGTG	2034
Db	2932	AAGTATCCACAAAAAGTGAAATTGCTAATGCCCCGGATGGAGCTGGGTCATTGCCTTGCA	2991
Qy	2035	CAGGATTGCCCCATGACCTTTCTTTCAAGAGTATACAACC-----TAAAGAGGAAGTTC	2088
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JOURNAL Cytogenet. Cell Genet. 88 (1-2), 101-102 (2000)
 MEDLINE 20237542
 PUBMED 10773680
 REFERENCE 2 (bases 1 to 4632)
 AUTHORS Zhou,Y., Yu,L. and Zhao,S.Y.
 TITLE Direct Submission
 JOURNAL Submitted (05-MAY-1999) Lab of Human Gene Research, Institute of
 Genetics, Fudan University, No. 220 Handan Rd., Shanghai 200433,
 P.R.China

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ORIGIN

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RESULT 10

AX195249

LOCUS AX195249 4053 bp RNA linear PAT 28-AUG-2001

DEFINITION Sequence 5 from Patent WO0151520.

ACCESSION AX195249

VERSION AX195249.1 GI:15385809

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Strittmatter, S.M.

TITLE Nogo receptor-mediated blockade of axonal growth

JOURNAL Patent: WO 0151520-A 5 19-JUL-2001;

YALE UNIVERSITY (US)

FEATURES

source

Location/Qualifiers

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CDS

135. .3713

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ORIGIN

Query Match 62.1%; Score 2379.4; DB 6; Length 4053;
 Best Local Similarity 86.6%; Pred. No. 0;
 Matches 2802; Conservative 0; Mismatches 381; Indels 54; Gaps 14;

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Qy	1797	GAGCTCAATACTGCAGTTTATTCAAGTGATGGCTTATTCATTGCTCAGGAAGCAAACCTA	1856
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Qy	1977	GTAGCCACAAAAGTGAAATTGCTGACATCCAGGATGGAGCTGGGTCATTGGCTTGTGCA	2036
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Qy	2871	GAAAGCCTGAAAGAGTTAACAATAGAGGAGTTTATCTTTAAAGGGGATATTCAATTTGATT	2930
Db	3714	AAACGCCCCAAAATAATTA-----GTAGGAGTTTCATCTTTAAAGGGGATATTCAATTTGATT	3768
Qy	2931	CCATTGGGGAGGGTCAGGGAAGAACAAGCCTTGACATTGCAGTGCAGTTTCAC-----	2984
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RESULT 11

AB020693

LOCUS AB020693 4053 bp mRNA linear PRI 16-JUN-1999

DEFINITION Homo sapiens mRNA for KIAA0886 protein, complete cds.

ACCESSION AB020693

VERSION AB020693.1 GI:4240260

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (sites)

AUTHORS Nagase,T., Ishikawa,K., Suyama,M., Kikuno,R., Hirose,M.,
Miyajima,N., Tanaka,A., Kotani,H., Nomura,N. and Ohara,O.

TITLE Prediction of the coding sequences of unidentified human genes.
XII. The complete sequences of 100 new cDNA clones from brain which
code for large proteins in vitro

JOURNAL DNA Res. 5 (6), 355-364 (1998)

MEDLINE 99156230

PUBMED 10048485

REFERENCE 2 (bases 1 to 4053)

AUTHORS Ohara,O., Suyama,M., Kikuno,R., Nagase,T. and Ishikawa,K.

TITLE Direct Submission

JOURNAL Submitted (02-DEC-1998) Osamu Ohara, Kazusa DNA Research Institute,
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Fax:+81-438-52-3914)

FEATURES

source

Location/Qualifiers

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gene

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CDS

135. .3713

/gene="KIAA0886"

/codon_start=1

/product="KIAA0886 protein"

/protein_id="BAA74909.1"

/db_xref="GI:4240261"

31 December 1998

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QY	601	AAAGATAGTGAAAGCAGTAATGATGACACTTCATTTCCCAGTACACCAGAAGCTGTAAGA	660
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Db	1500	GATCGTTTCAGGAGCATATATCACATGTGCTCCCTTTAACCCAGCAGCAACTGAGAGCATT	1559
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Qy 2091 GTCCCAGATGAGTTCTCCAAAGATAGGGGTGATGTTTCAAAGGTGCCCCTACTGCCTCCA 2150
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Db	3054	GTGAAAGAAGCTGAGAAAAACTTCCTTCCGATACAGAAAAAGAGGACAGATCACCATCT	3113
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polyA_signal 3402. .3407
ORIGIN

Query Match 62.1%; Score 2379.2; DB 9; Length 3491;
Best Local Similarity 86.4%; Pred. No. 0;
Matches 2806; Conservative 0; Mismatches 388; Indels 54; Gaps 14;

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Qy 1077 CTTTGCCCATCTTTTGAAGAATCTGAAGCTACTCCGTCACCGGTTTTGCCTGACATTGTC 1136
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Qy 1137 ATGGAAGCACCATTAAATTCTGTAGTTCCTAGTGCTGGTGCTTCTGCAGTGCAGCTCAGT 1196
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Qy 1197 TCATCACCATTAGAACTCTTCCTTCAGTTAATTATGAAAGCATAAAGTTTGAGCCTGAA 1256
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Qy 1317 GAAGAAATCACAGAGCCTGAAGGTATTAGTGTAGCTGTTGAGGAAACAGAAGCTCCTTAT 1376
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Qy	1377	ATATCTATTGCATGTGATTTAATTAAAGAAACAAAGATCTCTACTGAACCGACTCCAGAT	1436
Db	1643	ATATCTATTGCATGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAACCGACTCCGGAT	1702
Qy	1437	TTCTCTAGTTATTTCAGAAATAGCAGAAGTTGCACAGCCAGTGCCCGAGCATTCTGAGCTA	1496
Db	1703	TTCTCTGATTATTTCAGAAATGGCAAAGTTGAACAGCCAGTGCCTGATCATTCTGAGCTA	1762
Qy	1497	GTTGAAGATTCCCTCCCCGATTCTGAACCGATTGACTTATTTAGTGATGATTCAATACCC	1556
Db	1763	GTTGAAGATTCCCTCACCTGATTCTGAACCGATTGACTTATTTAGTGATGATTCAATACCT	1822
Qy	1557	GAAGTTCCACAAAAACAAGATGAAGCTGTAATACTTGTGAAAGAAAACCTCACTGAAATT	1616
Db	1823	GACGTTCCACAAAAACAAGATGAACTGTGATGCTTGTGAAAGAAAAGTCTCACTGAGACT	1882
Qy	1617	TCATCTGAGTCAATGACAGGACATGACAATAAGGGAAAACCTCAGTGCTTCACCATCACCT	1676
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Qy	1677	GAGGGAGGAAAACCGTATTTGGAGTCTTTTCAGCCAGTTTAGGCATCACAAAAGATACC	1736
Db	1940	GAGGGAGGAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATACC	1999
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Qy	1917	TTTGTGAGTTCTAAAGCAGATTCTTCTCCTACATTAGCCAGGGAATACACTGACCTAGAA	1976
Db	2180	TTGATCAGTTCTAAAACTGATTCATTTTCTAAATTAGCCAGGGAATATACTGACCTAGAA	2239
Qy	1977	GTAGCCACAAAAGTGAAATTGCTGACATCCAGGATGGAGCTGGGTGATTGGCTTGTGCA	2036
Db	2240	GTATCCACAAAAGTGAAATTGCTAATGCCCCGATGGAGCTGGGTGATTGCCTTGACACA	2299
Qy	2037	GGATTGCCCCATGACCTTTCTTTCAAGAGTATACAACCTA-----AAGAGGAAGTTCAT	2090
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Db	2480	GTGAAAGAAGCTGAGAAAAAACTTCCTTCCGATACAGAAAAAGAGGACAGATCACCATCT	2539
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Db	2600	ATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCCTATTTCCTGCTGCTTTCATTGACAGTA	2659
Qy	2391	TTCAGCATTGTGAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCTGTGACTATCAGC	2450
Db	2660	TTCAGCATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGC	2719
Qy	2451	TTTAGGATATATAAGGGTGTGATCCAGGCTATCCAGAAATCTGATGAAGGCCACCCATTC	2510
Db	2720	TTTAGGATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTC	2779
Qy	2511	AGGGCATATTTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGCAAT	2570
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Db	3020	ATTTATGAACGGCATCAGGCACAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTT	3079
Qy	2811	AAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGAATGA	2870
Db	3080	AAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCTGAATGA	3139
Qy	2871	GAAAGCCTGAAAGAGTTAACAATAGAGGAGTTTATCTTTAAAGGGGATATTCATTTGATT	2930
Db	3140	AAACGCCCCAAAATAATTA-----GTAGGAGTTCATCTTTAAAGGGGATATTCATTTGATT	3194
Qy	2931	CCATTGGGGAGGGTCAGGGAAGAACAAAGCCTTGACATTGCAGTGCAGTTTCAC-----	2984
Db	3195	ATACGGGGGAGGGTCAGGGAAGAACGAA-CCTTGACGTTGCAGTGCAGTTTCACAGATCG	3253
Qy	2985	-----AGATCTTTATTTTGTAGCAACGCAGTG-TCTGAGGAAAAATGACCTGTCTTGACTG	3038
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Qy	3039	CCCTGTGTTTCATCATCTTAAGTATTGTAAGCTGCTATGTATGGATTTAAATCGTAATCAT	3098

Db 3314 CCATGTGTTTCATCATCTTAAGTATTGTAAGCTGCTATGTATGGATTTAAACCGTAATCAT 3373
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 QY 3159 ACACTTTGTCGCAGGTAGTCTTGCTGTATTTGGGGAA-TTGCAAAGAAAGTGGAGCTGAC 3217
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RESULT 13

AB040462

LOCUS AB040462 4166 bp mRNA linear PRI 10-OCT-2001

DEFINITION Homo sapiens mRNA for RTN-xL, complete cds.

ACCESSION AB040462

VERSION AB040462.1 GI:11610574

KEYWORDS reticulon.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1

AUTHORS Tagami,S., Eguchi,Y., Kinoshita,M., Takeda,M. and Tsujimoto,Y.

TITLE A novel protein, RTN-XS, interacts with both Bcl-XL and Bcl-2 on endoplasmic reticulum and reduces their anti-apoptotic activity

JOURNAL Oncogene 19 (50), 5736-5746 (2000)

MEDLINE 21010696

PUBMED 11126360

REFERENCE

2 (bases 1 to 4166)

AUTHORS Eguchi,Y., Tagami,S. and Tsujimoto,Y.

TITLE Direct Submission

JOURNAL Submitted (22-MAR-2000) Yutaka Eguchi, Osaka University Graduate School of Medicine, Biomedical Research Center, Department of Medical Genetics; Yamadaoka 2-2, Suita, Osaka 567-0871, Japan (E-mail:eguchi@gene.med.osaka-u.ac.jp, Tel:+81-6-6879-3363, Fax:+81-6-6879-3369)

FEATURES

source

Location/Qualifiers

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CDS

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ORIGIN

Query Match 61.9%; Score 2372.6; DB 9; Length 4166;
 Best Local Similarity 86.2%; Pred. No. 0;
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Qy 481 AAAGATACTTACAAGCAAGATAGTGATGTTTTGATTGCTGGAGGTAATATAGAGAGCAAA 540
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Qy 661 GGTGGTTCCGGAGCGTACATCACGTGTGCTCCCTTTAACC---CAACAACGAGAATGTT 717
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Db 1610 GATCGTTCAGGAGCATATATCACATGTGCTCCCTTTAACCAGCAGCAACTGAGAGCATT 1669

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Qy 1017 AAAATGGACCTGGTTCAAACCTCAGAAGCTGTGCAGGAGTCACTTTACCCTGTAACACAG 1076
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Db 1970 AAAATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCACAG 2029

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Db 2030 CTTTGCCCATCATTTGAAGAGTCAGAAGCTACTCCTTCACCAGTTTTGCCTGACATTGTT 2089

Qy 1137 ATGGAAGCACCATTAAATTCTGTAGTTCCTAGTGCTGGTGCTTCTGCAGTGCAGCTCAGT 1196
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Db 2090 ATGGAAGCACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGATACAGCCCAGC 2149

Qy 1197 TCATCACCATTAGAACTCTTCCTTCAGTTAATTATGAAAGCATAAAGTTTGAGCCTGAA 1256
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Db 2150 TCATCACCATTAGAAGC---TTCTTCAGTTAATTATGAAAGCATAAAACATGAGCCTGAA 2206

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Qy 1437 TTCTCTAGTTATTCAGAAATAGCAGAAGTTGCACAGCCAGTGCCCGAGCATTCTGAGCTA 1496
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Qy 1917 TTTGTCAGTTCTAAAGCAGATTCTTCTCCTACATTAGCCAGGGAATACACTGACCTAGAA 1976
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Db	3404	TTTAGGATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTC	3463
Qy	2511	AGGGCATATTTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGCAAT	2570
Db	3464	AGGGCATATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGTAAT	3523
Qy	2571	TCTGCTCTTGGTCATGTTAACTGCACAATAAAAGAACTCAGACGCCTCTTCTTAGTTGAT	2630
Db	3524	TCTGCTCTTGGTCATGTGAAGTGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGAT	3583
Qy	2631	GATTTAGTTGATTCTCTGAAGTTTGCACTGTTGATGTGGGTATTTACCTATGTTGGTGCC	2690
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Qy	2811	AAAGATGCTATGGCTAAAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGAATGA	2870
Db	3764	AAAGATGCTATGGCTAAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCTGAATGA	3823
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Db	3824	AAACGCCCAAAATAATTA-----GTAGGAGTTCATCTTTAAAGGGGATATTCATTTGATT	3878
Qy	2931	CCATTGGGGAGGGTCAGGGAAGAACAAGCCTTGACATTGCAGTGCAGTTTCAC-----	2984
Db	3879	ATACGGGGGAGGGTCAGGGAAGAACGAA-CCTTGACGTTGCAGTGCAGTTTCACAGATCG	3937
Qy	2985	-----AGATCTTTATTTTTAGCAACGCAGTGT-CTGAGGAAAAATGACCTGTCTTGACTG	3038

Db	3938	TTGTTAGATCTTTATTTT TAGCCATGCACTGTTGTGAGGAAAAATTACCTGTCTTGACTG	3997
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Db	3998	CCATGTGTTTCATCATCTTAAGTATTGTAAGCTGCTATGTATGGATTTAAACCGTAATCAT	4057
Qy	3099	ATTTGTTTTTCTGTATGAGGCACTGGTGAATAAAACAAAGATCTGAGAAAGCTGTATATT	3158
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Qy	3159	ACACTTTGTGCGCAGGTAGTCTTGCTGTATTTGGGGAATT	3197
Db	4114	TTACTTTGTTGCAGATAGTCTTGCCGCATCTTGCCAAGT	4152

RESULT 14

BD270070

LOCUS BD270070 4093 bp DNA linear PAT 17-JUL-2003

DEFINITION Secreted proteins and polynucleotides encoding them.

ACCESSION BD270070

VERSION BD270070.1 GI:33079838

KEYWORDS JP 2002537757-A/32.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 4093)

AUTHORS Valenzuela, D., Yuan, O., Hoffman, H., Hall, J. and Rapiejko, P.

TITLE Secreted proteins and polynucleotides encoding them

JOURNAL Patent: JP 2002537757-A 32 12-NOV-2002;

ALPHAGENE INC

COMMENT	OS	Homo sapiens (human)
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PN JP 2002537757-A/32

PD 12-NOV-2002

PF 24-AUG-1999 JP 2000566287

PR 24-AUG-1998 US 60/097638, 24-AUG-1998 US 60/097659 PR

09-SEP-1998 US 60/099618, 28-SEP-1998 US 60/102092 PR

25-NOV-1998 US 60/109978,23-DEC-1998 US 60/113645 PR

23-DEC-1998 US 60/113646,23-AUG-1999 US 09/379246 PT DABTO

VALENZUELA, OLIVE YUAN, HEIDI HOFFMAN, JEFF HALL, PETER PI RAPIEJKO

PC C12N15/09,A61K38/00,A61K48/00,A61P3/10,A61P11/06,A61P21/00, PC
A61P29/00.

PC A61P31/04, A61P31/10, A61P31/12, A61P31/18, A61P35/00, A61P37/00,
PC C07K14/47.

PC C07K14/47,
PC C12N5/10,C12P21/02,G01N33/15,G01N33/50,C12N15/00,A61K37/02, PC
C12N5/00

CC	Secreted proteins and polynucleotides encoding them	FH	Key
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FEATURES	Location/Qualifiers
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ORIGIN

Query Match 61.8%; Score 2370.4; DB 6; Length 4093;
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Qy      61 GTACTGCCCCACTGAAGGAACACTTCCAGCAACTTCAAATGAAGCTTCTAAAGCATTCTCA 120
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Qy     361 GATAGAGTTCTGTCTCCAGAAAAAACAAAGGACAGTTTAAAGGAAAAGGGAGTTGCAGCA 420
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Qy     421 GAAGCTTCTATGGGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTG 480
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Db    1279 GAAGCTCCTATGAGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTG 1338

Qy     481 AAAGATACTTACAAGCAAGATAGTGATGTTTTGATTGCTGGAGGTAATATAGAGAGCAAA 540
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Qy     541 TTGGAAGGTAAAGTGGATAAGAAACACTTTTCAGATAGCCTTGAACAAACAAATCGTGAA 600
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[illegible]

Db	2473	TCATTTGAGTCAATGATAGAATATGAAAATAAGGAAAACTCAGTGCTTTGC---CACCT	2529
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Qy	1737	TTAGCACCTGATGAAGTTTCAGCATTGACCCAAAAGGAGAAAATCCCTTTGCAGATGGAG	1796
Db	2590	CTGTTACCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAATTCCTTTGCAGATGGAG	2649
Qy	1797	GAGCTCAATACTGCAGTTTATTCAAGTGATGGCTTATTGCTCAGGAAGCAAACCTA	1856
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Qy	1857	AGAGAAAGTGAAACATTTTCAGATTTCATCTCCGATTGAGATTATAGATGAGTTCCCGACC	1916
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Db	2830	GTATCCACAAAAGTGAAATTGCTAATGCCCGGATGGAGCTGGGTCATTGCCTTGCACA	2889
Qy	2037	GGATTGCCCATGACCTTTCTTTCAAGAGTATACAACCTA-----AAGAGGAAGTTCAT	2090
Db	2890	GAATTGCCCATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCAGT	2949
Qy	2091	GTCCCAGATGAGTTCTCCAAAGATAGGGGTGATGTTTCAAAGGTGCCCGTACTGCCTCCA	2150
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Qy	2211	GTGAAAGAAGCCGAGAGAAAACCTTCCTTCTGATACAGAAAAAGAGCGAAGATCTCCATCT	2270
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LOCUS BD249446 3579 bp DNA linear PAT 17-JUL-2003
 DEFINITION Protein similar to neuroendocrine-specific protein, and encoding cDNA.
 ACCESSION BD249446
 VERSION BD249446.1 GI:33059216
 KEYWORDS JP 2002522016-A/1.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 3579)
 AUTHORS Michalovich, D. and Prinjha, R.K.
 TITLE Protein similar to neuroendocrine-specific protein, and encoding
 JOURNAL Patent: JP 2002522016-A 1 23-JUL-2002;
 SMITHKLINE BEECHAM PLC
 COMMENT OS Homo sapiens (human)
 PN JP 2002522016-A/1
 PD 23-JUL-2002
 PF 21-JUL-1999 JP 2000561310
 PR 22-JUL-1998 GB 9816024.5, 19-JUL-1999 GB 9916898.1 PI
 DAVID MICHALOVICH, RABINDER KUMAR PRINJHA
 PC C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/10, PC
 C12P21/02, C12Q1/02, C12Q1/68, G01N33/15, G01N33/50, G01N33/53, PC
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 PC C12P21/08, C12N15/00, C12N5/00
 CC Protein similar to neuroendocrine-specific protein, and encoding cDNA
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QY 301 AACATCCTTCATACTCAGCAGGAGTTATCTACAGTCCTTACGAAATCAGTTGAAGAAGAA 360
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QY 421 GAAGCTTCTATGGGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTG 480
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Db 1129 GAAGCTCCTATGAGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTG 1188
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Db 1546 AACCCCTTTCCTTGTAGCAGCACAGGATTCTGAGACAGATTATGTCACAACAGATAATTTA 1605
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QY	1257	AATCCCCCACCATATGAGGAGGCCATGAATGTATCACTAAAAAAGAATCAGGAATGAAT	1316
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Db	2263	GACGTTCCACAAAAACAAGATGAAACTGTGATGCTTGTGAAAGAAAGTCTCACTGAGACT	2322
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Db	2380	GAGGGAGGAAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATAACC	2439
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Db	2440	CTGTTACCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAATTCCTTTGCAGATGGAG	2499
QY	1797	GAGCTCAATACTGCAGTTTATTCAAGTGATGGCTTATTCATTGCTCAGGAAGCAAACCTA	1856
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QY	1857	AGAGAAAGTGAAACATTTTCAGATTTCATCTCCGATTGAGATTATAGATGAGTTCCCGACC	1916
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QY	1917	TTTGTTCAGTTCTAAAGCAGATTCTTCTCCTACATTAGCCAGGGAATACACTGACCTAGAA	1976
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Db	2680	GTATCCCACAAAAGTGAAATTGCTAATGCCCCGATGGAGCTGGGTCAATTGCCTTGCACA	2739
QY	2037	GGATTGCCCCATGACCTTTCTTTCAAGAGTATACAACC-----TAAAGAGGAAGTTCAT	2090
Db	2740	GAATTGCCCCATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCAGT	2799
QY	2091	GTCCCGAGATGAGTTCTCCAAAGATAGGGGTGATGTTTCAAAGGTGCCCGTACTGCCTCCA	2150
Db	2800	TTCTCAGATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCA	2859
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QY	2211	GTGAAAGAAGCCGAGAGAAAACCTTCCTTCTGATACAGAAAAGAGCGAAGATCTCCATCT	2270
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QY	2271	GCTATATTTTCAGCAGAGCTGAGTAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGAC	2330
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QY	2331	ATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCTTGTTCCTGCTGCTCTCGCTGACAGTA	2390
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Db	3220	AGGGCATATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTTCAAGTACAGTAAT	3279
QY	2571	TCTGCTCTTGGTCATGTAACTGCACAATAAAAGAACTCAGACGCCTCTTCTTAGTTGAT	2630
Db	3280	TCTGCTCTTGGTCATGTGAAGTGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGAT	3339
QY	2631	GATTTAGTTGATTCTCTGAAGTTTGCAGTGTGATGTGGGTATTTACCTATGTTGGTGCC	2690
Db	3340	GATTTAGTTGATTCTCTGAAGTTTGCAGTGTGATGTGGGTATTTACCTATGTTGGTGCC	3399
QY	2691	TTGTTCAATGGTCTGACACTACTAATTTTGGCTCTGATTTCACTCTTCAGTGTTCCTGTT	2750
Db	3400	TTGTTTAATGGTCTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTTCCTGTT	3459
QY	2751	ATTTATGAACGGCATCAGGCGCAAATAGATCATTATCTGGGACTTGCAAATAAGAATGTT	2810

Db 3460 |||||ATTTATGAACGGCATCAGGCGCAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTT 3519
Qy 2811 AAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGAATGA 2870
Db 3520 AAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCTGAATGA 3579

Search completed: September 11, 2004, 10:10:22
Job time : 14434.6 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 10, 2004, 23:36:15 ; Search time 1342.11 Seconds
(without alignments)
12132.674 Million cell updates/sec

Title: US-09-830-972-28
Perfect score: 3833
Sequence: 1 ctatctcctctctcagccgc.....ttaaaaaaaaaaaaaaaaaaaaa 3833

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_29Jan04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002s:*
7: geneseqn2003as:*
8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	3833	100.0	3833	3	AAD01174	Aad01174 Bovine ne
2	2687.8	70.1	4822	6	ABS70449	Abs70449 Human bon
3	2649.8	69.1	4632	6	ABV94680	Abv94680 Human pan
4	2566.4	67.0	4698	7	ABX34563	Abx34563 Human mdd
5	2379.4	62.1	4053	4	AAS09453	Aas09453 Human cDN
6	2379.4	62.1	4053	8	ACC81048	Acc81048 Human Nog
7	2370.4	61.8	4093	3	AAA23454	Aaa23454 cDNA enco

	8	2223.6	58.0	3579	3	AAZ56886	Aaz56886 Human MAG
	9	2223.6	58.0	3579	4	AAF90324	Aaf90324 Human NOG
	10	2223.6	58.0	3579	6	ABK90134	Abk90134 DNA encod
	11	2223.6	58.0	3579	6	ABN86601	Abn86601 Human neu
	12	2183.4	57.0	4684	3	AAD01173	Aad01173 Rat neur
	13	2179.4	56.9	4684	6	ABN86600	Abn86600 Rat neuro
	14	1777.2	46.4	2386	2	AAV30920	Aav30920 Human sec
	15	1774	46.3	2386	5	AAF98399	Aaf98399 Human cDN
	16	1414.6	36.9	1980	4	AAI98079	Aai98079 Human neu
c	17	1039.8	27.1	1758	4	AAF32725	Aaf32725 Human sec
	18	1031.8	26.9	2240	3	AAC64406	Aac64406 Human Nog
	19	1025.4	26.8	2235	6	ABV94681	Abv94681 Human pan
	20	989.2	25.8	1514	6	ABK34580	Abk34580 Human cDN
	21	986	25.7	1798	6	ABK90135	Abk90135 DNA encod
	22	827.2	21.6	2052	6	ABK90133	Abk90133 DNA encod
	23	826.4	21.6	2782	9	ADB85284	Adb85284 Rat fooce
	24	750.4	19.6	1568	3	AAD01175	Aad01175 Rat neur
	25	685.8	17.9	1213	2	AAX04379	Aax04379 Human sec
	26	685.8	17.9	1610	3	AAZ36230	Aaz36230 cDNA enco
	27	681.4	17.8	991	2	AAX97587	Aax97587 Extended
	28	681.2	17.8	1694	4	AAK94408	Aak94408 Human ful
	29	590.8	15.4	799	2	AAV23695	Aav23695 Human NSP
	30	573.4	15.0	770	3	AAA72983	Aaa72983 Human NSP
	31	573.4	15.0	1216	6	ABA05903	Aba05903 Human RTN
	32	552.4	14.4	2100	7	ABT42936	Abt42936 Human neu
	33	539	14.1	1683	4	AAD08386	Aad08386 Human sec
	34	538.8	14.1	868	3	AAZ56887	Aaz56887 Human MAG
c	35	535	14.0	4710	4	AAL04697	Aal04697 Human rep
c	36	535	14.0	4710	4	ABL97604	Ab197604 Human tes
	37	527	13.7	600	4	AAF90323	Aaf90323 Human NOG
	38	527	13.7	1122	3	AAZ56888	Aaz56888 Human MAG
	39	527	13.7	1122	4	AAF90325	Aaf90325 Human NOG
	40	464	12.1	472	7	ABX50578	Abx50578 Bovine ES
	41	463.4	12.1	3535	4	AAH72837	Aah72837 Human cer
	42	427.2	11.1	447	7	ABX50261	Abx50261 Bovine ES
	43	427	11.1	441	7	ABX53872	Abx53872 Bovine ES
	44	423.8	11.1	429	7	ABX53062	Abx53062 Bovine ES
	45	422	11.0	422	7	ABX43312	Abx43312 Bovine ES

ALIGNMENTS

RESULT 1

AAD01174

ID AAD01174 standard; cDNA; 3833 BP.

XX

AC AAD01174;

XX

DT 02-NOV-2000 (first entry)

XX

DE Bovine neurite growth inhibitor Nogo cDNA.

XX

KW Bovine; neurite growth inhibitor; Nogo; neural cell; myelin; CNS;
KW central nervous system; neoplastic disease; antiproliferative; glioma;
KW antisense gene therapy; neuroblastoma; menagioma; retinoblastoma;
KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;

Db 1 CTATCTCCTCTCTCAGCCGCTGCTTTTAAAGAACGTGAATACCTTGGTGATTTACCAGCA 60
 Qy 61 GTACTGCCCCACTGAAGGAACACTTCCAGCAACTTCAAATGAAGCTTCTAAAGCATTCTCA 120
 Db 61 GTACTGCCCCACTGAAGGAACACTTCCAGCAACTTCAAATGAAGCTTCTAAAGCATTCTCA 120
 Qy 121 GAGAAGGCCAAAAATCCATTTGTAGAGAGAAATTTAACAGAATTTTCAGAATTGGAATAT 180
 Db 121 GAGAAGGCCAAAAATCCATTTGTAGAGAGAAATTTAACAGAATTTTCAGAATTGGAATAT 180
 Qy 181 TCAGAAATGGAATCATCATTTCAGTGGCTCTCAAAGGCAGAACCTGCCGTAACAGTAGCG 240
 Db 181 TCAGAAATGGAATCATCATTTCAGTGGCTCTCAAAGGCAGAACCTGCCGTAACAGTAGCG 240
 Qy 241 AATCCTAGGGACGAAATAGTTGTGAGGAGTAGAGATAAAGAAGAGGACTTAGTTAGTCTT 300
 Db 241 AATCCTAGGGACGAAATAGTTGTGAGGAGTAGAGATAAAGAAGAGGACTTAGTTAGTCTT 300
 Qy 301 AACATCCTTCATACTCAGCAGGAGTTATCTACAGTCCTTACGAAATCAGTTGAAGAAGAA 360
 Db 301 AACATCCTTCATACTCAGCAGGAGTTATCTACAGTCCTTACGAAATCAGTTGAAGAAGAA 360
 Qy 361 GATAGAGTTCTGTCTCCAGAAAAACAAAGGACAGTTTAAAGGAAAAGGGAGTTGCAGCA 420
 Db 361 GATAGAGTTCTGTCTCCAGAAAAACAAAGGACAGTTTAAAGGAAAAGGGAGTTGCAGCA 420
 Qy 421 GAAGCTTCTATGGGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTG 480
 Db 421 GAAGCTTCTATGGGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTG 480
 Qy 481 AAAGATACTTACAAGCAAGATAGTGATGTTTTGATTGCTGGAGGTAATATAGAGAGCAAA 540
 Db 481 AAAGATACTTACAAGCAAGATAGTGATGTTTTGATTGCTGGAGGTAATATAGAGAGCAAA 540
 Qy 541 TTGGAAGGTAAAGTGGATAAGAAACACTTTTCAGATAGCCTTGAACAAACAAATCGTGAA 600
 Db 541 TTGGAAGGTAAAGTGGATAAGAAACACTTTTCAGATAGCCTTGAACAAACAAATCGTGAA 600
 Qy 601 AAAGATAGTGAAAGCAGTAATGATGACACTTCATTTCCAGTACACCAGAAGCTGTAAGA 660
 Db 601 AAAGATAGTGAAAGCAGTAATGATGACACTTCATTTCCAGTACACCAGAAGCTGTAAGA 660
 Qy 661 GGTGGTTCCGGAGCGTACATCACGTGTGCTCCCTTTAACCCAACAACAGAGAATGTTTCA 720
 Db 661 GGTGGTTCCGGAGCGTACATCACGTGTGCTCCCTTTAACCCAACAACAGAGAATGTTTCA 720
 Qy 721 ACAAACATTTTCCCTTGTGGAAGATCATACTTCGAAAATAAGACAGATGAAAAAAG 780
 Db 721 ACAAACATTTTCCCTTGTGGAAGATCATACTTCGAAAATAAGACAGATGAAAAAAG 780
 Qy 781 ATAGAAAAAAAAGGCACAAATTGTAACAGAGAAGAATGCAAGTGTCAAGACATCAAACC 840
 Db 781 ATAGAAAAAAAAGGCACAAATTGTAACAGAGAAGAATGCAAGTGTCAAGACATCAAACC 840
 Qy 841 CTTTCCTTATGGCAGCACAGGAGTCTAAGACAGATTACGTTACAACAGATCATGTGTCAA 900
 Db 841 CTTTCCTTATGGCAGCACAGGAGTCTAAGACAGATTACGTTACAACAGATCATGTGTCAA 900

Qy	901	AGGTGACCGAGGAAGTAGTGGCAAACATGCCTGAAGGTCTAACCCAGATTTGGTTCAGG	960
Db	901	AGGTGACCGAGGAAGTAGTGGCAAACATGCCTGAAGGTCTAACCCAGATTTGGTTCAGG	960
Qy	961	AAGCATGTGAAAGTGAATTGAATGAAGCTACTGGTACAAAAATTGCCTTTGAAACAAAAA	1020
Db	961	AAGCATGTGAAAGTGAATTGAATGAAGCTACTGGTACAAAAATTGCCTTTGAAACAAAAA	1020
Qy	1021	TGGACCTGGTTCAAACTTCAGAAGCTGTGCAGGAGTCACTTTACCCTGTAACACAGCTTT	1080
Db	1021	TGGACCTGGTTCAAACTTCAGAAGCTGTGCAGGAGTCACTTTACCCTGTAACACAGCTTT	1080
Qy	1081	GCCCATCTTTTGAAGAATCTGAAGCTACTCCGTCACCGGTTTTGCCTGACATTGTCATGG	1140
Db	1081	GCCCATCTTTTGAAGAATCTGAAGCTACTCCGTCACCGGTTTTGCCTGACATTGTCATGG	1140
Qy	1141	AAGCACCATTAAATTCTGTAGTTCCTAGTGCTGGTGCTTCTGCAGTGCAGCTCAGTTCAT	1200
Db	1141	AAGCACCATTAAATTCTGTAGTTCCTAGTGCTGGTGCTTCTGCAGTGCAGCTCAGTTCAT	1200
Qy	1201	CACCATTAGAAACTCTTCCTTCAGTTAATTATGAAAGCATAAAGTTTGAGCCTGAAAATC	1260
Db	1201	CACCATTAGAAACTCTTCCTTCAGTTAATTATGAAAGCATAAAGTTTGAGCCTGAAAATC	1260
Qy	1261	CCCCACCATATGAGGAGGCCATGAATGTATCACTAAAAAAGAATCAGGAATGAATGAAG	1320
Db	1261	CCCCACCATATGAGGAGGCCATGAATGTATCACTAAAAAAGAATCAGGAATGAATGAAG	1320
Qy	1321	AAATCACAGAGCCTGAAGGTATTAGTGTAGCTGTTTCAGGAAACAGAAGCTCCTTATATAT	1380
Db	1321	AAATCACAGAGCCTGAAGGTATTAGTGTAGCTGTTTCAGGAAACAGAAGCTCCTTATATAT	1380
Qy	1381	CTATTGCATGTGATTTAATTAAAGAAACAAAGATCTCTACTGAACCGACTCCAGATTTCT	1440
Db	1381	CTATTGCATGTGATTTAATTAAAGAAACAAAGATCTCTACTGAACCGACTCCAGATTTCT	1440
Qy	1441	CTAGTTATTCAGAAATAGCAGAAGTTGCACAGCCAGTGCCCCGAGCATTCTGAGCTAGTTG	1500
Db	1441	CTAGTTATTCAGAAATAGCAGAAGTTGCACAGCCAGTGCCCCGAGCATTCTGAGCTAGTTG	1500
Qy	1501	AAGATTCTCCCCGATTCTGAACCAAGTTGACTTATTTAGTGATGATTCAATACCCGAAG	1560
Db	1501	AAGATTCTCCCCGATTCTGAACCAAGTTGACTTATTTAGTGATGATTCAATACCCGAAG	1560
Qy	1561	TTCCACAAAAACAAGATGAAGCTGTAATACTTGTGAAAGAAAACCTCACTGAAATTTTCAT	1620
Db	1561	TTCCACAAAAACAAGATGAAGCTGTAATACTTGTGAAAGAAAACCTCACTGAAATTTTCAT	1620
Qy	1621	CTGAGTCAATGACAGGACATGACAATAAGGGAAAACCTCAGTGCTTCACCATCACCTGAGG	1680
Db	1621	CTGAGTCAATGACAGGACATGACAATAAGGGAAAACCTCAGTGCTTCACCATCACCTGAGG	1680
Qy	1681	GAGGAAAACCGTATTTGGAGTCTTTTCAGCCCAGTTTAGGCATCACAAAAGATACCTTAG	1740
Db	1681	GAGGAAAACCGTATTTGGAGTCTTTTCAGCCCAGTTTAGGCATCACAAAAGATACCTTAG	1740

Qy	1741	CACCTGATGAAGTTTTCAGCATTGACCCAAAAGGAGAAAAATCCCTTTGCAGATGGAGGAGC	1800
Db	1741	CACCTGATGAAGTTTTCAGCATTGACCCAAAAGGAGAAAAATCCCTTTGCAGATGGAGGAGC	1800
Qy	1801	TCAATACTGCAGTTTATTCAAGTGATGGCTTATTCATTGCTCAGGAAGCAAACCTAAGAG	1860
Db	1801	TCAATACTGCAGTTTATTCAAGTGATGGCTTATTCATTGCTCAGGAAGCAAACCTAAGAG	1860
Qy	1861	AAAGTGAAACATTTTCAGATTTCATCTCCGATTGAGATTATAGATGAGTTCCCGACCTTTG	1920
Db	1861	AAAGTGAAACATTTTCAGATTTCATCTCCGATTGAGATTATAGATGAGTTCCCGACCTTTG	1920
Qy	1921	TCAGTTCTAAAGCAGATTCTTCTCCTACATTAGCCAGGGAATACACTGACCTAGAAGTAG	1980
Db	1921	TCAGTTCTAAAGCAGATTCTTCTCCTACATTAGCCAGGGAATACACTGACCTAGAAGTAG	1980
Qy	1981	CCCACAAAAGTGAAATTGCTGACATCCAGGATGGAGCTGGGTTCATTGGCTTGTGCAGGAT	2040
Db	1981	CCCACAAAAGTGAAATTGCTGACATCCAGGATGGAGCTGGGTTCATTGGCTTGTGCAGGAT	2040
Qy	2041	TGCCCCATGACCTTTCTTTCAAGAGTATACAACCTAAAGAGGAAGTTCATGTCCCAGATG	2100
Db	2041	TGCCCCATGACCTTTCTTTCAAGAGTATACAACCTAAAGAGGAAGTTCATGTCCCAGATG	2100
Qy	2101	AGTTCTCCAAAGATAGGGGTGATGTTTCAAAGGTGCCCGTACTGCCTCCAGATGTTTCTG	2160
Db	2101	AGTTCTCCAAAGATAGGGGTGATGTTTCAAAGGTGCCCGTACTGCCTCCAGATGTTTCTG	2160
Qy	2161	CTTTGGATGCTCAAGCAGAGATAGGCAGCATAGAAAAACCCAAAGTTCTTGTGAAAGAAG	2220
Db	2161	CTTTGGATGCTCAAGCAGAGATAGGCAGCATAGAAAAACCCAAAGTTCTTGTGAAAGAAG	2220
Qy	2221	CCGAGAGAAAACCTTCCTTCTGATACAGAAAAAGAGCGAAGATCTCCATCTGCTATATTTT	2280
Db	2221	CCGAGAGAAAACCTTCCTTCTGATACAGAAAAAGAGCGAAGATCTCCATCTGCTATATTTT	2280
Qy	2281	CAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAGAAGA	2340
Db	2281	CAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAGAAGA	2340
Qy	2341	CTGGAGTGGTGTGTTGGTGCCAGCTTGTTTCCTGCTGCTCTCGCTGACAGTATTCAGCATTG	2400
Db	2341	CTGGAGTGGTGTGTTGGTGCCAGCTTGTTTCCTGCTGCTCTCGCTGACAGTATTCAGCATTG	2400
Qy	2401	TGAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATAT	2460
Db	2401	TGAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATAT	2460
Qy	2461	ATAAGGGTGTGATCCAGGCTATCCAGAAATCTGATGAAGGCCACCCATTTCAGGGCATATT	2520
Db	2461	ATAAGGGTGTGATCCAGGCTATCCAGAAATCTGATGAAGGCCACCCATTTCAGGGCATATT	2520
Qy	2521	TGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTTCAGAAGTACAGCAATTCTGCTCTTG	2580
Db	2521	TGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTTCAGAAGTACAGCAATTCTGCTCTTG	2580
Qy	2581	GTCATGTAACTGCACAATAAAAGAACTCAGACGCCTCTTCTTAGTTGATGATTTAGTTG	2640

Db	2581	 GTCATGTTAACTGCACAATAAAAGAACTCAGACGCCTCTTCTTAGTTGATGATTTAGTTG	2640
Qy	2641	ATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTCAATG	2700
Db	2641	 ATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTCAATG	2700
Qy	2701	GTCTGACACTACTAATTTTGGCTCTGATTTCACTCTTCAGTGTTCCCTGTTATTTATGAAC	2760
Db	2701	 GTCTGACACTACTAATTTTGGCTCTGATTTCACTCTTCAGTGTTCCCTGTTATTTATGAAC	2760
Qy	2761	GGCATCAGGCGCAAATAGATCATTATCTGGGACTTGCAAATAAGAATGTTAAAGATGCTA	2820
Db	2761	 GGCATCAGGCGCAAATAGATCATTATCTGGGACTTGCAAATAAGAATGTTAAAGATGCTA	2820
Qy	2821	TGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGAATGAGAAAGCCTGA	2880
Db	2821	 TGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGAATGAGAAAGCCTGA	2880
Qy	2881	AAGAGTTAACAATAGAGGAGTTTATCTTTAAAGGGGATATTCATTTGATTCCATTGGGGA	2940
Db	2881	 AAGAGTTAACAATAGAGGAGTTTATCTTTAAAGGGGATATTCATTTGATTCCATTGGGGA	2940
Qy	2941	GGGTCAGGGAAGAACAAGCCTTGACATTGCAGTGCAGTTTCACAGATCTTTATTTTATAG	3000
Db	2941	 GGGTCAGGGAAGAACAAGCCTTGACATTGCAGTGCAGTTTCACAGATCTTTATTTTATAG	3000
Qy	3001	CAACGCAGTGTCTGAGGAAAAATGACCTGTCTTGACTGCCCTGTGTTTCATCATCTTAAGT	3060
Db	3001	 CAACGCAGTGTCTGAGGAAAAATGACCTGTCTTGACTGCCCTGTGTTTCATCATCTTAAGT	3060
Qy	3061	ATTGTAAGCTGCTATGTATGGATTTAAATCGTAATCATATTTGTTTTTCTGTATGAGGC	3120
Db	3061	 ATTGTAAGCTGCTATGTATGGATTTAAATCGTAATCATATTTGTTTTTCTGTATGAGGC	3120
Qy	3121	ACTGGTGAATAAAACAAAGATCTGAGAAAGCTGTATATTACACTTTGTGCGAGGTAGTCTT	3180
Db	3121	 ACTGGTGAATAAAACAAAGATCTGAGAAAGCTGTATATTACACTTTGTGCGAGGTAGTCTT	3180
Qy	3181	GCTGTATTTGGGGAATTGCAAAGAAAGTGGAGCTGACAGAAATAACCCTTTTCACAGTTT	3240
Db	3181	 GCTGTATTTGGGGAATTGCAAAGAAAGTGGAGCTGACAGAAATAACCCTTTTCACAGTTT	3240
Qy	3241	GTGCACTGTGTACGGTCTGTGTAGGTTGATGCAGATTTTCTGAAATGAAATGTTTAGACG	3300
Db	3241	 GTGCACTGTGTACGGTCTGTGTAGGTTGATGCAGATTTTCTGAAATGAAATGTTTAGACG	3300
Qy	3301	AGATCATGCCACCAAGGCAGGAGTGAAAAAGCTTGCCTTTCTGGTATGTTCTAGGTGTA	3360
Db	3301	 AGATCATGCCACCAAGGCAGGAGTGAAAAAGCTTGCCTTTCTGGTATGTTCTAGGTGTA	3360
Qy	3361	TTGTGAAATTTACTGTTGTATTAATTGCCAATATAAGTAAATATAGATTATATATATCTA	3420
Db	3361	 TTGTGAAATTTACTGTTGTATTAATTGCCAATATAAGTAAATATAGATTATATATATCTA	3420
Qy	3421	TATATAGTGTTTCACGAAGCTTAGCCCTTTACCTTCCCAGCTGCCCCACAGTGCTTGATA	3480

Db 3421 TATATAGTGTTCACGAAGCTTAGCCCTTTACCTTCCCAGCTGCCCCACAGTGCTTGATA 3480
 Qy 3481 CTTCTGTCATGGGTTTTATGTGTGTAGTCCCAAAGCACATAAGCTAGGGAGAAACGTACT 3540
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 3481 CTTCTGTCATGGGTTTTATGTGTGTAGTCCCAAAGCACATAAGCTAGGGAGAAACGTACT 3540
 Qy 3541 TCTAGGCGCACTACCATCTGTTTTCAACACGAACCGACGCCATGCAAACAGAACTCCTCA 3600
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 3541 TCTAGGCGCACTACCATCTGTTTTCAACACGAACCGACGCCATGCAAACAGAACTCCTCA 3600
 Qy 3601 ACATAAACTTCACTGCACAGACTTACTGTAGTTAATTTTATCACAAACTCTGGACTGAAT 3660
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 3601 ACATAAACTTCACTGCACAGACTTACTGTAGTTAATTTTATCACAAACTCTGGACTGAAT 3660
 Qy 3661 CTAATGCTTCCAAAAATGTTTGCAAATATCAAACATTGTTATGTAAGAAAAATATAAATGA 3720
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 3661 CTAATGCTTCCAAAAATGTTTGCAAATATCAAACATTGTTATGTAAGAAAAATATAAATGA 3720
 Qy 3721 CGATTTATACAATTGTGGTTTAAGCTGTATTGAACTAAATCTGTGGAATGCATTGTGAAC 3780
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 3721 CGATTTATACAATTGTGGTTTAAGCTGTATTGAACTAAATCTGTGGAATGCATTGTGAAC 3780
 Qy 3781 TGTAAAAGCAAAGTATCAATAAAGCTTATAGACTTAAAAAAAAAAAAAAAAAAAAA 3833
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 3781 TGTAAAAGCAAAGTATCAATAAAGCTTATAGACTTAAAAAAAAAAAAAAAAAAAAA 3833

RESULT 2

ABS70449

ID ABS70449 standard; cDNA; 4822 BP.

XX

AC ABS70449;

XX

DT 27-NOV-2002 (first entry)

XX

DE Human bone remodelling gene #106.

XX

KW Bone remodelling; osteoporosis; human; gene; ss.

XX

OS Homo sapiens.

XX

PN US6426186-B1.

XX

PD 30-JUL-2002.

XX

PF 18-JAN-2000; 2000US-00484970.

XX

PR 18-JAN-2000; 2000US-00484970.

XX

PA (INCY-) INCYTE GENOMICS INC.

XX

PI Jones KA, Volkmuth W, Walker MG;

XX

DR WPI; 2002-673014/72.

XX

PT A combination of polynucleotides which are co-expressed with genes known
 PT to be involved in bone remodeling and osteoporosis are useful in an array

Qy	601	AAAGATAGTGAAAGCAGTAATGATGACACTTCATTTCCCGAGTACACCAGAAGCTGTAAGA	660
Db	1558	AAAGATAGTGAGAGTAGTAATGATGATACTTCTTTCCCCAGTACGCCAGAAGGTATAAAG	1617
Qy	661	GGTGGTTCCGGAGCGTACATCACGTGTGCTCCCTTTAACC---CAACAACCTGAGAATGTT	717
Db	1618	GATCGTTTCAGGAGCATATATCACATGTGCTCCCTTTAACCAGCAGCAACTGAGAGCATT	1677
Qy	718	TCAACAAACATTTTTCCCTTGTTGGAAGATCATACTTCGGAAAATAAGACAGATGAAAAA	777
Db	1678	GCAACAAACATTTTTCTTTGTTAGGAGATCCTACTTCAGAAAATAAGACCGATGAAAAA	1737
Qy	778	AAGA--TAGAAAAAAAAAGGCACAAATTGTAACAGAGAAGAATGCAAGTGTCAAGACATC	835
Db	1738	AAAAATAGAAGAAAAGAAGGCCCAAATAGTAACAGAGAAGAATACTAGCACCAAACATC	1797
Qy	836	AAACCC-TTTCCTTATGGCAGCACAGGAGTCTAAGACAGATTACGTTACAACAGATCATG	894
Db	1798	AAACCCCTTTTACTTGTAGCAGCACAGGATTCTGAGACAGATTATGTCACAACAGATAATT	1857
Qy	895	TGTCAAAGGTGACCGAGGAAGTAGTGGCAAACATGCCTGAAGGTCTAACCCAGATTTGG	954
Db	1858	TAACAAAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCCAGATTTAG	1917
Qy	955	TTCAGGAAGCATGTGAAAGTGAATTGAATGAAGCTACTGGTACAAAATTGCCTTTGAAA	1014
Db	1918	TACAGGAAGCATGTGAAAGTGAATTGAATGAAGTTACTGGTACAAAGATTGCTTATGAAA	1977
Qy	1015	CAAAAATGGACCTGGTTCAAACCTCAGAAAGCTGTGCAGGAGTCACTTTACCCTGTAACAC	1074
Db	1978	CAAAAATGGACTTGGTTCAAACATCAGAAGTATGCAAGAGTCACTCTATCCTGCAGCAC	2037
Qy	1075	AGCTTTGCCCATCTTTTGAAGAATCTGAAGCTACTCCGTCACCGGTTTTGCCTGACATTG	1134
Db	2038	AGCTTTGCCCATCATTTGAAGAGTCAGAAGCTACTCCTTCACCAGTTTTGCCTGACATTG	2097
Qy	1135	TCATGGAAGCACCATTAAATTCTGTAGTTCCTAGTGCTGGTGCTTCTGCAGTGCAGCTCA	1194
Db	2098	TTATGGAAGCACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGATACAGCCCA	2157
Qy	1195	GTTCATCACCATTAGAACTCTTCCTTCAGTTAATTATGAAAGCATAAAGTTTGAGCCTG	1254
Db	2158	GCTCATCACCATTAGAAGC---TTCCTTCAGTTAATTATGAAAGCATAAAACATGAGCCTG	2214
Qy	1255	AAAATCCCCCACCATATGAGGAGGCCATGAATGTATCACTAAAAAAGAATCAGGAATGA	1314
Db	2215	AAAACCCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAGTATCAGGAATAA	2274
Qy	1315	ATGAAGAAATCACAGAGCCTGAAGGTATTAGTGTAGCTGTTCAGGAAACAGAAGCTCCTT	1374
Db	2275	AGGAAGAAATTAAAGAGCCTGAAAATATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTT	2334
Qy	1375	ATATATCTATTGCATGTGATTTAATTAAAGAAACAAAGATCTCTACTGAACCGACTCCAG	1434
Db	2335	ATATATCTATTGCATGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAACCGACTCCGG	2394

Qy	1435	ATTTCTCTAGTTATTTCAGAAATAGCAGAAGTTGCACAGCCAGTGCCCGAGCATTCTGAGC	1494
Db	2395	ATTTCTCTGATTATTTCAGAAATGGCAAAGTTGAACAGCCAGTGCCTGATCATTCTGAGC	2454
Qy	1495	TAGTTGAAGATTCTCTCCCCGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATAC	1554
Db	2455	TAGTTGAAGATTCTCTCACCTGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATAC	2514
Qy	1555	CCGAAGTTCCACAAAAACAAGATGAAGCTGTAATACTTGTGAAAGAAAACCTCACTGAAA	1614
Db	2515	CTGACGTTCCACAAAAACAAGATGAACTGTGATGCTTGTGAAAGAAAAGTCTCACTGAGA	2574
Qy	1615	TTTCATCTGAGTCAATGACAGGACATGACAATAAGGGAAAACTCAGTGCTTCACCATCAC	1674
Db	2575	CTTCATTTGAGTCAATGATAGAATATGAAAAAAGGAAAAACTCAGTGCTTTGC---CAC	2631
Qy	1675	CTGAGGGAGGAAAACCGTATTTGGAGTCTTTTCAGCCCAGTTTAGGCATCACAAAAGATA	1734
Db	2632	CTGAGGGAGGAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATA	2691
Qy	1735	CCTTAGCACCTGATGAAGTTTCAGCATTGACCCAAAAGGAGAAAATCCCTTTGCAGATGG	1794
Db	2692	CCCTGTTACCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAATTCCTTTGCAGATGG	2751
Qy	1795	AGGAGCTCAATACTGCAGTTTATTCAAGTGATGGCTTATTCATTGCTCAGGAAGCAAACC	1854
Db	2752	AGGAGCTCAGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGA	2811
Qy	1855	TAAGAGAAAGTGAACATTTTCAGATTTCATCTCCGATTGAGATTATAGATGAGTTCCCGA	1914
Db	2812	TAAGAGAAACTGAAACGTTTTTCAGATTTCATCTCCAATTGAAATTATAGATGAGTTCCCTA	2871
Qy	1915	CCTTTGTGAGTTCTAAAGCAGATTCTTCTCCTACATTAGCCAGGGAATACACTGACCTAG	1974
Db	2872	CATTGATCAGTTCTAAAAC TGATT CATTTTCTAAATTAGCCAGGGAATATACTGACCTAG	2931
Qy	1975	AAGTAGCCACAAAAGTGAAATTGCTGACATCCAGGATGGAGCTGGGTGATTGGCTTGTG	2034
Db	2932	AAGTATCCACAAAAGTGAAATTGCTAATGCCCCGATGGAGCTGGGTGATTGCCTTGCA	2991
Qy	2035	CAGGATTGCCCCATGACCTTTCTTTCAAGAGTATACAACC-----TAAAGAGGAAGTTC	2088
Db	2992	CAGAATTGCCCCATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCA	3051
Qy	2089	ATGTCCCAGATGAGTTCTCCAAAGATAGGGGTGATGTTTCAAAGGTGCCCGTACTGCCTC	2148
Db	3052	GTTTCTCAGATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTC	3111
Qy	2149	CAGATGTTTCTGCTTTGGATGCTCAAGCAGAGATAGGCAGCATAGAAAAACCCAAAGTTC	2208
Db	3112	CAGATGTTTCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTC	3171
Qy	2209	TTGTGAAAGAAGCCGAGAGAAAACCTCCTTCTGATACAGAAAAAGAGCGAAGATCTCCAT	2268
Db	3172	TTGTGAAAGAAGCTGAGAAAAAACCTCCTTCCGATACAGAAAAAGAGGACAGATCACCAT	3231
Qy	2269	CTGCTATATTTTCAGCAGAGCTGAG-TAAAACCTCAGTTGTTGACCTCCTCTACTGGAGA	2327

Db	3232	CTGCTATATTTTCAGCAGAGCTGAGCTAAAACTTCAGTTGTTGACCTCCTGTACTGGAGA	3291
Qy	2328	GACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCTTGTTCTGCTGCTCTCGCTGACA	2387
Db	3292	GACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCCTATTCCTGCTGCTTTCATTGACA	3351
Qy	2388	GTATTCAGCATTTGTGAGTGTAACGGCCTACATTGCCTTGCCCTGCTCTCTGTGACTATC	2447
Db	3352	GTATTCAGCATTTGTGAGCGTAACAGCCTACATTGCCTTGCCCTGCTCTCTGTGACCATC	3411
Qy	2448	AGCTTTAGGATATATAAGGGTGTGATCCAAGGCTATCCAGAAATCTGATGAAGGCCACCCA	2507
Db	3412	AGCTTTAGGATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCA	3471
Qy	2508	TTCAGGGCATATTTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGC	2567
Db	3472	TTCAGGGCATATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGT	3531
Qy	2568	AATTCTGCTCTTGGTCATGTAACTGCACAATAAAAGAACTCAGACGCCTCTTCTTAGTT	2627
Db	3532	AATTCTGCTCTTGGTCATGTGAAGTGCACGATAAAGGAAGTTCAGGCGCCTCTTCTTAGTT	3591
Qy	2628	GATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGT	2687
Db	3592	GATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGT	3651
Qy	2688	GCCTTGTTCAATGGTCTGACACTACTAATTTTGGCTCTGATTTCACTCTTCAGTGTTCCCT	2747
Db	3652	GCCTTGTTTAAATGGTCTGACACTACTGATTTTGGCTCTCATTTCACCTTCAGTGTTCCCT	3711
Qy	2748	GTTATTTATGAACGGCATCAGGCGCAAATAGATCATTATCTGGGACTTGCAAATAAGAAT	2807
Db	3712	GTTATTTATGAACGGCATCAGGCACAGATAGATCATTATCTAGGACTTGCAAATAAGAAT	3771
Qy	2808	GTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGAA	2867
Db	3772	GTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGAA	3831
Qy	2868	TGAGAAAGCCTGAAAGAGTTAACAATAGAGGAGTTTATCTTTAAAGGGGATATTCATTTG	2927
Db	3832	TGAAAACGCCCAAATAATTA-----GTAGGAGTTCATCTTTAAAGGGGATATTCATTTG	3886
Qy	2928	ATTCATTGGGGAGGGTCAGGGAAGAACAAGCCTTGACATTGCAGTGCAGTTTCAC---	2984
Db	3887	ATTATACGGGGAGGGTCAGGGAAGAACGAA-CCTTGACGTTGCAGTGCAGTTTCACAGA	3945
Qy	2985	-----AGATCTTTATTTTTAGCAACGCAGTG-TCTGAGGAAAAATGACCTGTCTTGA	3035
Db	3946	TCGTTGTTAGATCTTTATTTTTAGCCATGCACTGTTGTGAGGAAAAATTACCTGTCTTGA	4005
Qy	3036	CTGCCCTGTGTTTCATCATCTTAAGTATTGTAAGCTGCTATGTATGGATTTAAATCGTAAT	3095
Db	4006	CTGCCATGTGTTTCATCATCTTAAGTATTGTAAGCTGCTATGTATGGATTTAAACCGTAAT	4065
Qy	3096	CATATTTGTTTTTCCTGTATGAGGCACTGGTGAATAAACAAAGATCTGAGAAAGCTGTAT	3155

DT 14-JAN-2003 (first entry)
 XX
 DE Human pancreatic cancer expressed cDNA SEQ ID NO 53.
 XX
 KW Human; pancreas; cancer; gene therapy; vaccine; immunostimulant;
 KW cytostatic; tumour; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200260317-A2.
 XX
 PD 08-AUG-2002.
 XX
 PF 30-JAN-2002; 2002WO-US002781.
 XX
 PR 30-JAN-2001; 2001US-0265305P.
 PR 31-JAN-2001; 2001US-0265682P.
 PR 09-FEB-2001; 2001US-0267568P.
 PR 21-MAR-2001; 2001US-0278651P.
 PR 28-APR-2001; 2001US-0287112P.
 PR 16-MAY-2001; 2001US-0291631P.
 PR 12-JUL-2001; 2001US-0305484P.
 PR 20-AUG-2001; 2001US-0313999P.
 PR 27-NOV-2001; 2001US-0333626P.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Benson DR, Kalos MD, Lodes MJ, Persing DH, Hepler WT, Jiang Y;
 XX
 DR WPI; 2002-627435/67.
 DR P-PSDB; ABP68600.
 XX
 PT New isolated polynucleotide and pancreatic tumor polypeptides, useful for
 PT diagnosing, preventing and/or treating cancer, particularly pancreatic
 PT cancer.
 XX
 PS Claim 1; SEQ ID NO 53; 300pp + Sequence Listing; English.
 XX
 CC The invention relates to an isolated polynucleotide (I) comprising: (a)
 CC any of a group of over 4000 nucleotide sequences (ABV94628-ABV99145); (b)
 CC complements of (a); (c) sequences consisting of at least 20 contiguous
 CC residues of (a); (d) sequences that hybridize to (a), under moderately
 CC stringent conditions; (e) sequences having at least 75% or 90% identity
 CC to (a); or (f) degenerate variants of (a). Polypeptides (ABP68596-
 CC ABP68637) encoded by (I) and oligonucleotide can be used to detect cancer
 CC in a patient and compositions comprising polypeptides, polynucleotides,
 CC antibodies, fusion proteins, T cell populations and antigen presenting
 CC cells expressing the polypeptide are useful in treating pancreatic cancer
 CC and stimulating an immune response. The polynucleotides can be used as
 CC probes or primers for nucleic acid hybridisation, in the design and
 CC preparation of ribozyme molecules for inhibiting expression of the tumour
 CC polypeptides and proteins in the tumour cells, in vaccines and for gene
 CC therapy. Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 4632 BP; 1398 A; 1013 C; 1011 G; 1210 T; 0 U; 0 Other;

Query Match 69.1%; Score 2649.8; DB 6; Length 4632;
Best Local Similarity 85.0%; Pred. No. 0;
Matches 3292; Conservative 0; Mismatches 442; Indels 137; Gaps 24;

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Qy      1 CTATCTCCTCTCTCAGCCGCTGCTTTTAAAGAACGTGAATACCTTGGTGATTTACCAGCA 60
      || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    853 CTGTCTCCTCTCTCAGCCGCTTCTTTCAAAGAACATGAATACCTTGGTAATTTGTCAACA 912

Qy      61 GTACTGCCCCACTGAAGGAACACTTCCAGCAACTTCAAATGAAGCTTCTAAAGCATTTCTCA 120
      ||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    913 GTATTACCCACTGAAGGAACACTTCAAGAAAATGTCAGTGAAGCTTCTAAAGAGGTCTCA 972

Qy     121 GAGAAGGCCAAAAATCCATTTGTAGAGAGAAATTTAACAGAATTTTCAGAATTGGAATAT 180
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    973 GAGAAGGCCAAAACTCTACTCATAGATAGAGATTTAACAGAGTTTTCAGAATTAGAATAC 1032

Qy     181 TCAGAAATGGAATCATCATTTCAGTGGCTCTCAAAGGCAGAACCTGCCGTAACAGTAGCG 240
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db   1033 TCAGAAATGGGATCATCGTTTCAGTGTCTCTCCAAAAGCAGAATCTGCCGTAATAGTAGCA 1092

Qy     241 AATCCTAGGGACGAAATAGTTGTGAGGAGTAGAGATAAAGAAGAGGACTTAGTTAGTCTT 300
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db   1093 AATCCTAGGGAAGAAATAATCGTGAAAAATAAAGATGAAGAAGAGAAGTTAGTTAGTAAT 1152

Qy     301 AACATCCTTCATACTCAGCAGGAGTTATCTACAGTCCTTACGAAATCAGTTGAAGAAGAA 360
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db   1153 AACATCCTTCATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGGTTAAAGAGGAT 1212

Qy     361 GATAGAGTTCTGTCTCCAGAAAAAACAAAGGACAGTTTAAAGGAAAAGGGAGTTGCAGCA 420
      || |||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db   1213 GA---AGTTGTGTCTTCAGAAAAAGCAAAGACAGTTTAAATGAAAAGAGAGTTGCAGTG 1269

Qy     421 GAAGCTTCTATGGGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTG 480
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db   1270 GAAGCTCCTATGAGGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTG 1329

Qy     481 AAAGATACTTACAAGCAAGATAGTGATGTTTTGATTGCTGGAGGTAATATAGAGAGCAAA 540
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db   1330 AAAGATAGT---AAGGAAGATAGTGATATGTTGGCTGCTGGAGGTAATATCGAGAGCAAC 1386

Qy     541 TTGGAAGGTAAAGTGGATAAGAAACACTTTTTCAGATAGCCTTGAACAAACAAATCGTGAA 600
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db   1387 TTGGAAGGTAAAGTGGATAAAAAATGTTTTGCAGATAGCCTTGAACAACTAATCACGAA 1446

Qy     601 AAAGATAGTGAAAGCAGTAATGATGACACTTCATTTCCCAGTACACCAGAAGCTGTAAGA 660
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db   1447 AAAGATAGTGAGAGTAGTAATGATGATACTTCTTTCCCAGTACGCCAGAAGGTATAAAG 1506

Qy     661 GGTGGTTCCGGAGCGTACATCACGTGTGCTCCCTTTAACC---CAACAACAGAGAATGTT 717
      | | |||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db   1507 GATCGTTCAGGAGCATATATCACATGTGCTCCCTTTAACCAGCAGCAACTGAGAGCATT 1566

Qy     718 TCAACAAACATTTTTCCTTGTGGAAGATCATACTTCGGAATAAGACAGATGAAAAA 777
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db   1567 GCAACAAACATTTTTCCTTGTGGAAGATCATACTTCAGAAAATAAGACCGATGAAAAA 1626
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Qy	778	AAGATAGAA-AAAAAAGGCCACAAATTGTAAACAGAGAAGAATGCAAGTGTCAAGACATCA	836
Db	1627	AAAATAGAAGAAAAGAAGGCCCAAATAGTAACAGAGAAGAATACTAGCACCAAACATCA	1686
Qy	837	AACCCTTTCCTTATGGCAGCACAGGAGTCTAAGACAGATTACGTTACAACAGATCATGTG	896
Db	1687	AACCCTTTCCTTGTAGCAGCACAGGATTCTGAGACAGATTATGTCAACAGATAATTTA	1746
Qy	897	TCAAAGGTGACCGAGGAAGTAGTGGCAAACATGCCTGAAGGTCTAACCCCAGATTTGGTT	956
Db	1747	ACAAAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCCAGATTTAGTA	1806
Qy	957	CAGGAAGCATGTGAAAGTGAATTGAATGAAGCTACTGGTACAAAAATTGCCTTTGAAACA	1016
Db	1807	CAGGAAGCATGTGAAAGTGAATTGAATGAAGTTACTGGTACAAAGATTGCTTATGAAACA	1866
Qy	1017	AAAATGGACCTGGTTCAAACTTCAGAAGCTGTGCAGGAGTCACTTTACCCTGTAACACAG	1076
Db	1867	AAAATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCACAG	1926
Qy	1077	CTTGCCCATCTTTTGAAGAATCTGAAGCTACTCCGTCACCGGTTTTGCCTGACATTGTC	1136
Db	1927	CTTGCCCATCATTTGAAGAGTCAGAAGCTACTCCTTCACCAGTTTTGCCTGACATTGTT	1986
Qy	1137	ATGGAAGCACCATTAAATTCTGTAGTTCCTAGTGCTGGTGCTTCTGCAGTGCAGCTCAGT	1196
Db	1987	ATGGAAGCACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGATACAGCCCAGC	2046
Qy	1197	TCATCACCATTAGAAACTCTTCCTTCAGTTAATTATGAAAGCATAAAGTTTGAGCCTGAA	1256
Db	2047	TCATCACCATTAGAAGC---TTCTTCAGTTAATTATGAAAGCATAAAACATGAGCCTGAA	2103
Qy	1257	AATCCCCCACCATATGAGGAGGCCATGAATGTATCACTAAAAAAGAATCAGGAATGAAT	1316
Db	2104	AACCCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAGTATCAGGAATAAAG	2163
Qy	1317	GAAGAAATCACAGAGCCTGAAGGTATTAGTGTAGCTGTTTCAGGAAACAGAAGCTCCTTAT	1376
Db	2164	GAAGAAATTAAAGAGCCTGAAAATATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTAT	2223
Qy	1377	ATATCTATTGCATGTGATTTAATTAAAGAAACAAAGATCTCTACTGAACCGACTCCAGAT	1436
Db	2224	ATATCTATTGCATGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAACCAGCTCCGGAT	2283
Qy	1437	TTCTCTAGTTATTTCAGAAATAGCAGAAGTTGCACAGCCAGTGCCTGAGCATTCTGAGCTA	1496
Db	2284	TTCTCTGATTATTTCAGAAATGGCAAAGTTGAACAGCCAGTGCCTGATCATTCTGAGCTA	2343
Qy	1497	GTTGAAGATTCCCTCCCCGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCC	1556
Db	2344	GTTGAAGATTCCCTCACCTGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCT	2403
Qy	1557	GAAGTTCCACAAAAACAAGATGAAGCTGTAATACTTGTGAAAGAAAACCTCACTGAAATT	1616
Db	2404	GACGTTCCACAAAAACAAGATGAACTGTGATGCTTGTGAAAGAAAGTCTCACTGAGACT	2463
Qy	1617	TCATCTGAGTCAATGACAGGACATGACAATAAGGGAAAACCTCAGTGCTTCACCATCACCT	1676

Db	2464	TCATTTGAGTCAATGATAGAATATGAAAATAAGGAAAAACTCAGTGCTTTGC---CACCT	2520
Qy	1677	GAGGGAGGAAAACCGTATTTGGAGTCTTTTCAGCCCAGTTTAGGCATCACAAAAGATACC	1736
Db	2521	GAGGGAGGAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATACC	2580
Qy	1737	TTAGCACCTGATGAAGTTTCAGCATTGACCCAAAAGGAGAAAATCCCTTTGCAGATGGAG	1796
Db	2581	CTGTTACCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAATTCCTTTGCAGATGGAG	2640
Qy	1797	GAGCTCAATACTGCAGTTTATTCAAGTGATGGCTTATTCATTGCTCAGGAAGCAAACCTA	1856
Db	2641	GAGCTCAGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGATA	2700
Qy	1857	AGAGAAAAGTGAAACATTTTCAGATTTCATCTCCGATTGAGATTATAGATGAGTTCCCGACC	1916
Db	2701	AGAGAAACTGAAACGTTTTCAGATTTCATCTCCAATTGAAATTATAGATGAGTTCCCTACA	2760
Qy	1917	TTTGTGAGTTCTAAAGCAGATTCTTCTCCTACATTAGCCAGGGAATACACTGACCTAGAA	1976
Db	2761	TTGATCAGTTCTAAAACTGATTTCATTTCTAAATTAGCCAGGGAATATACTGACCTAGAA	2820
Qy	1977	GTAGCCACAAAAGTGAAATTGCTGACATCCAGGATGGAGCTGGGTTCATTGGCTTGTGCA	2036
Db	2821	GTATCCACAAAAGTGAAATTGCTAATGCCCGGATGGAGCTGGGTTCATTGCCTTGACACA	2880
Qy	2037	GGATTGCCCCATGACCTTTCTTTCAAGAGTATACAACC-----TAAAGAGGAAGTTCAT	2090
Db	2881	GAATTGCCCCATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCAGT	2940
Qy	2091	GTCCCAGATGAGTTCTCCAAAGATAGGGGTGATGTTTCAAAGGTGCCCGTACTGCCTCCA	2150
Db	2941	TTCTCAGATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCA	3000
Qy	2151	GATGTTTCTGCTTTGGATGCTCAAGCAGAGATAGGCAGCATAGAAAAACCCAAAGTTCTT	2210
Db	3001	GATGTTTCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTT	3060
Qy	2211	GTGAAAGAAGCCGAGAGAAAACCTCCTTCTGATACAGAAAAAGAGCGAAGATCTCCATCT	2270
Db	3061	GTGAAAGAAGCTGAGAAAAAACTCCTTCCGATACAGAAAAAGAGGACAGATCACCATCT	3120
Qy	2271	GCTATATTTTTCAGCAGAGCTGAGTAAAACCTTCAGTTGTTGACCTCCTCTACTGGAGAGAC	2330
Db	3121	GCTATATTTTTCAGCAGAGCTGAGTAAAACCTTCAGTTGTTGACCTCCTGTACTGGAGAGAC	3180
Qy	2331	ATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCTTGTTTCCTGCTGCTCTCGCTGACAGTA	2390
Db	3181	ATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCCTATTCTGCTGCTTTTCATTGACAGTA	3240
Qy	2391	TTCAGCATTGTGAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCTGTGACTATCAGC	2450
Db	3241	TTCAGCATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGC	3300
Qy	2451	TTTAGGATATATAAGGGTGTGATCCAGGCTATCCAGAAATCTGATGAAGGCCACCCATTC	2510

Db 3301 TTTAGGATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTC 3360

Qy 2511 AGGGCATATTTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGCAAT 2570
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Db 3361 AGGGCATATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGTAAT 3420

Qy 2571 TCTGCTCTTGGTCATGTAACTGCACAATAAAAGAACTCAGACGCCTCTTCTTAGTTGAT 2630
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Db 3421 TCTGCTCTTGGTCATGTGAAGTGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGAT 3480

Qy 2631 GATTTAGTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCC 2690
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Db 3481 GATTTAGTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCC 3540

Qy 2691 TTGTTCAATGGTCTGACACTACTAATTTTGGCTCTGATTTCACTCTTCAGTGTTCCCTGTT 2750
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Db 3541 TTGTTTAATGGTCTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTTCCCTGTT 3600

Qy 2751 ATTTATGAACGGCATCAGGCGCAAATAGATCATTATCTGGGACTTGCAAATAAGAATGTT 2810
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Db 3601 ATTTATGAACGGCATCAGGCACAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTT 3660

Qy 2811 AAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGAATGA 2870
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Db 3661 AAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCTGAATGA 3720

Qy 2871 GAAAGCCTGAAAGAGTTAACAATAGAGGAGTTTATCTTTAAAGGGGATATTCATTTGATT 2930
 || ||| ||| ||| |||||

Db 3721 AAACGCCCAAAATAAATTAGT-----AGGAGTTCATCTTTAAAGGGGATATTCATTTGATT 3775

Qy 2931 CCATTGGGGAGGGTCAGGGAAGAACAAAGCCTTGACATTGCAGTGCAGTTTACAGATCT 2990
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Db 3776 AT-----ACGGATCT 3785

Qy 2991 TTATTTTTAGCAACGCAGTG-TCTGAGGAAAAATGACCTGTCTTGACTGCCCTGTGTTCA 3049
 ||||| ||| ||| |||||

Db 3786 TTATTTTTAGCCATGCACTGTTGTGAGGAAAAATTACCTGTCTTGACTGCCATGTGTTCA 3845

Qy 3050 TCATCTTAAGTATTGTAAGCTGCTATGTATGGATTTAAATCGTAATCATATTTGTTTTTC 3109
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Db 3846 TCATCTTAAGTATTGTAAGCTGCTATGTATGGATTTAAACCGTAATCATA--TCTTTTTTC 3903

Qy 3110 CTGTATGAGGCACTGGTGAATAAACAAGATCTGAGAAAGCTGTATATTACACTTTGTCTG 3169
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Db 3904 CTATCTGAGGCACTGGTGGG-----ATAAAAAACCTGTATATTTTACTTTGTTG 3952

Qy 3170 CAGGTAGTCTTGCTGTAT-TTGGGGAATTGCAAAGAAAGTGGAGCT-----GACAGAAA 3222
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Db 3953 CAGATAGTCTTGCCGCATCTTGGCAAGTTGCAGAGATGGTGGAGCTAGAAAAAAAAAAAAA 4012

Qy 3223 TAACCCTTTTTCACAGTTTGTGCACTGTGTACGGTCTGTGTAGGTTGATGCAGATTTTCTG 3282
 || | ||| ||||| ||||| ||||| |||||

Db 4013 AAAAGCCCTTTTCAGTTTGTGCACTGTGTATGGTCCGTGTAGATTGATGCAGATTTTCTG 4072

Qy 3283 AAATGAAA----TGTTTAGACGAGATCATGCCACCAAGGCAGGAGTGAAAAAGCTTGCCCT 3338
 ||||| ||||| ||| ||| ||||| |||

Db 4073 AAATGAAATGTTTGTTTAGACGAGATCATACCGGTAAAGCAGGAATGACAAAGCTTG-CT 4131

OS Homo sapiens.
XX
PN WO200279449-A2.
XX
PD 10-OCT-2002.
XX
PF 27-MAR-2002; 2002WO-US009944.
XX
PR 28-MAR-2001; 2001US-0279619P.
PR 29-MAR-2001; 2001US-0280067P.
PR 29-MAR-2001; 2001US-0280068P.
PR 16-MAY-2001; 2001US-0291280P.
PR 17-MAY-2001; 2001US-0291829P.
PR 17-MAY-2001; 2001US-0291849P.
PR 19-JUN-2001; 2001US-0299428P.
PR 20-JUN-2001; 2001US-0299776P.
PR 20-JUN-2001; 2001US-0300001P.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;
PI Dufour GE, Hillman JL, Yu JY, Tuason O, Yap PE, Amshey SR;
PI Daugherty SC, Dam TC, Liu TF, Nguyen DA, Kleefeld Y, Gerstin EH;
PI Peralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;
PI Flores V, Marwaha R, Lo A, Lan RY, Urashka ME;
XX
DR WPI; 2003-058431/05.
DR P-PSDB; ABU11573.
XX
PT New purified disease detection and treatment molecule proteins and
PT polynucleotides, useful for diagnosing, treating or preventing cancers
PT (e.g. leukemia or sarcoma), anemia, Crohn's disease, AIDS, osteoporosis
PT or hepatitis.
XX
PS Claim 1; SEQ ID NO 124; 339pp + Sequence Listing; English.
XX
CC This invention describes a novel disease detection and treatment molecule
CC polypeptide (MDDT) which has anti-inflammatory, immunosuppressive,
CC osteopathic, cytostatic, anti-HIV, haemostatic, nephrotropic,
CC antianaemic, antipsoriatic and hepatotropic activity. The polynucleotides
CC and the polypeptides of the invention can be used for gene therapy,
CC protein replacement therapy and are useful for treating a variety of
CC diseases or conditions. These polypeptides or polynucleotides are
CC particularly useful for diagnosing, treating or preventing cell
CC proliferative disorders (e.g. cancers including adenocarcinoma,
CC leukaemia, lymphoma, melanoma, myeloma or sarcoma), anaemia, Crohn's
CC disease, acquired immunodeficiency syndrome (AIDS), Goodpasture's
CC syndromes, inflammation, osteoporosis, thrombocytopaenia, psoriasis or
CC hepatitis. ABX34440-ABX34835 encode the MDDT polypeptides represented in
CC ABU11450-ABU11845, described in the disclosure of the invention. NOTE:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 4698 BP; 1410 A; 1028 C; 1022 G; 1238 T; 0 U; 0 Other;

Query Match

67.0%; Score 2566.4; DB 7; Length 4698;

Best Local Similarity 84.7%; Pred. No. 0;
Matches 3221; Conservative 0; Mismatches 441; Indels 140; Gaps 25;

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Qy      1 CTATCTCCTCTCTCAGCCGCTGCTTTTAAAGAACGTGAATACCTTGGTGATTTACCAGCA 60
      || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      856 CTGTCTCCTCTCTCAGCCGCTTCTTCAAAGAACATGAATACCTTGGTAATTTGTCAACA 915

Qy      61 GTACTGCCCCACTGAAGGAACACTTCCAG-CAACTTCAAATGAAGCTTCTAAAGCATTCTC 119
      ||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      916 GTATTACCCACTGAAGGAACACTTCAAGAAAAATGTCAGTGAAGCTTCTAAAGAGGTCTC 975

Qy     120 AGAGAAGGCAAAAAATCCATTTGTAGAGAGAAAATTTAACAGAAATTTTCAGAATTGGAATA 179
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db     976 AGAGAAGGCAAAAACTCTACTCATAGATAGAGATTTAACAGAGTTTTCAGAATTAGAATA 1035

Qy     180 TTCAGAAATGGAATCATTCATTGAGTGGCTCTCAAAGGCAGAACCTGCCGTAACAGTAGC 239
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    1036 CTCAGAAATGGGATCATCGTTGAGTGTCTCTCCAAAGCAGAAATCTGCCGTAATAGTAGC 1095

Qy     240 GAATCCTAGGGACGAAATAGTTGTGAGGAGTAGAGATAAAGAAGAGGACTTAGTTAGTCT 299
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    1096 AAATCCTAGGGAAGAAATAATCGTGAAAAATAAAGATGAAGAAGAGAAGTTAGTTAGTAA 1155

Qy     300 TAACATCCTTCATACTCAGCAGGAGTTATCTACAGTCCTTACGAAATCAGTTGAAGAAGA 359
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    1156 TAACATCCTTCATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGGTTAAAGAGGA 1215

Qy     360 AGATAGAGTTCTGTCTCCAGAAAAAACAAAGGACAGTTTTTAAGGAAAAGGGAGTTGCAGC 419
      || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    1216 TGA---AGTTGTGTCTTCAGAAAAAGCAAAAGACAGTTTTTAATGAAAAGAGAGTTGCAGT 1272

Qy     420 AGAAGCTTCTATGGGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGT 479
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    1273 GGAAGCTCCTATGAGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGT 1332

Qy     480 GAAAGATACTTACAAGCAAGATAGTGATGTTTTGATTGCTGGAGGTAATATAGAGAGCAA 539
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    1333 GAAAGATAGT---AAGGAAGATAGTGATATGTTGGCTGCTGGAGGTAAAATCGAGAGCAA 1389

Qy     540 ATTGGAAGGTAAAGTGGATAAGAAACACTTTTCAGATAGCCTTGAACAAACAAATCGTGA 599
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    1390 CTTGGAAAGTAAAGTGGATAAAAAATGTTTTGCAGATAGCCTTGAGCAAACATAATCACGA 1449

Qy     600 AAAAGATAGTGAAAGCAGTAATGATGACACTTCATTTCCCAGTACACCAGAAGCTGTAAG 659
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    1450 AAAAGATAGTGAGAGTAGTAATGATGATACTTCTTTCCCAGTACGCCAGAAGGTATAAA 1509

Qy     660 AGGTGGTTCCGGAGCGTACATCACGTGTGCTCCCTTTAACC---CAACAACGAGAATGT 716
      | | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    1510 GGATCGTTCAGGAGCATATATCACATGTGCTCCCTTTAACCAGCAGCAACTGAGAGCAT 1569

Qy     717 TTCAACAAACATTTTTCCCTTGTTGGAAGATCATACTTCGGAAAATAAGACAGATGAAAA 776
      | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    1570 TGCAACAAACATTTTTCCCTTGTTAGGAGATCCTACTTCAGAAAATAAGACCGATGAAAA 1629

Qy     777 AAAGATAGAA-AAAAAAAGGCACAAATTGTAACAGAGAAGAATGCAAGTGTCAAGACATC 835
      ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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Db 1630 AAAAATAGAAGAAAAGAAGGCCCAAATAGTAACAGAGAAGAATACTAGCACCAAAACATC 1689

Qy 836 AAACCCCTTTCCTTATGGCAGCACAGGAGTCTAAGACAGATTACGTTACAACAGATCATGT 895
 ||||| ||| ||||| ||| ||||| ||| ||||| |||

Db 1690 AAACCCCTTTCCTTGTAGCAGCACAGGATTCTGAGACAGATTATGTCACAACAGATAATTT 1749

Qy 896 GTCAAAGGTGACCGAGGAAGTAGTGGCAAACATGCCTGAAGGTCTAACCCAGATTGTTGGT 955
 ||||| ||||| ||||| ||||| ||||| ||| ||| ||||| |||

Db 1750 AACAAAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCCAGATTTAGT 1809

Qy 956 TCAGGAAGCATGTGAAAAGTGAATTGAATGAAGCTACTGGTACAAAAATTGCCTTTGAAAC 1015
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 1810 ACAGGAAGCATGTGAAAAGTGAATTGAATGAAGTTACTGGTACAAAGATTGCTTATGAAAC 1869

Qy 1016 AAAAATGGACCTGGTTCAAACCTTCAGAAGCTGTGCAGGAGTCACTTTACCTGTAAACACA 1075
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Db 1870 AAAAATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCACA 1929

Qy 1076 GCTTTGCCCATCTTTTGAAGAATCTGAAGCTACTCCGTCACCGGTTTTGCCTGACATTGT 1135
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 1930 GCTTTGCCCATCATTTGAAGAGTCAGAAGCTACTCCTTCACCAGTTTTGCCTGACATTGT 1989

Qy 1136 CATGGAAGCACCATTAAATTCTGTAGTTCCTAGTGCTGGTGCTTCTGCAGTGCAGCTCAG 1195
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 1990 TATGGAAGCACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGATACAGCCAG 2049

Qy 1196 TTCATCACCATTAGAAACTCTTCCTTCAGTTAATTATGAAAGCATAAAAGTTTGAGCCTGA 1255
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Db 2050 CTCATCACCATTAGAAAGC---TTCTTCAGTTAATTATGAAAGCATAAAACATGAGCCTGA 2106

Qy 1256 AAATCCCCCACCATATGAGGAGGCCATGAATGTATCACTAAAAAAGAATCAGGAATGAA 1315
 ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 2107 AAACCCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAGTATCAGGAATAAA 2166

Qy 1316 TGAAGAAATCACAGAGCCTGAAGGTATTAGTGTAGCTGTTTCAGGAAACAGAAGCTCCTTA 1375
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 2167 GGAAGAAATTAAGAGCCTGAAAATATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTA 2226

Qy 1376 TATATCTATTGCATGTGATTTAATTAAAGAAACAAAGATCTCTACTGAACCGACTCCAGA 1435
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Db 2227 TATATCTATTGCATGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAACAGCTCCGGA 2286

Qy 1436 TTTCTCTAGTTATTCAGAAATAGCAGAAGTTGCACAGCCAGTGCCCGAGCATTCTGAGCT 1495
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 2287 TTTCTCTGATTATTCAGAAATGGCAAAAGTTGAACAGCCAGTGCCTGATCATTCTGAGCT 2346

Qy 1496 AGTTGAAGATTCTCCCCCGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACC 1555
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 2347 AGTTGAAGATTCTCACCTGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACC 2406

Qy 1556 CGAAGTTCCACAAAAACAAGATGAAGCTGTAATACTTGTGAAAGAAAACCTCACTGAAAT 1615
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Db 2407 TGACGTTCCACAAAAACAAGATGAAACTGTGATGCTTGTGAAAGAAAGTCTCACTGAGAC 2466

Qy 1616 TTCATCTGAGTCAATGACAGGACATGACAATAAGGGAAAACCTCAGTGCTTACCATCACC 1675
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 2467 TTCATTTGAGTCAATGATAGAATATGAAAATAAGGAAAACCTCAGTGCTTTGC---CACC 2523

Qy	1676	TGAGGGAGGAAAACCGTATTTGGAGTCTTTTCAGCCCAGTTTAGGCATCACAAAAGATAC	1735
Db	2524	TGAGGGAGGAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATAC	2583
Qy	1736	CTTAGCACCTGATGAAGTTTCAGCATTGACCCAAAAGGAGAAAATCCCTTTGCAGATGGA	1795
Db	2584	CCTGTTACCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAATTCCTTTGCAGATGGA	2643
Qy	1796	GGAGCTCAATACTGCAGTTTATTCAAGTGATGGCTTATTCATTGCTCAGGAAGCAAACCT	1855
Db	2644	GGAGCTCAGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGAT	2703
Qy	1856	AAGAGAAAGTGAAACATTTTCAGATTTCATCTCCGATTGAGATTATAGATGAGTTCCCGAC	1915
Db	2704	AAGAGAAACTGAAACGTTTTCAGATTTCATCTCAATTGAAATTATAGATGAGTTCCCTAC	2763
Qy	1916	CTTTGTCTAGTTCTAAAGCAGATTCTTCTCCTACATTAGCCAGGGAATACACTGACCTAGA	1975
Db	2764	ATTGATCAGTTCTAAAACTGATTCAATTTCTAAATTAGCCAGGGAATATACTGACCTAGA	2823
Qy	1976	AGTAGCCACAAAAGTGAAATTGCTGACATCCAGGATGGAGCTGGGTCATTGGCTTGTGC	2035
Db	2824	AGTATCCACAAAAGTGAAATTGCTAATGCCCGGATGGAGCTGGGTCATTGCCTTGCAC	2883
Qy	2036	AGGATTGCCCCATGACCTTTCTTTCAAGAGTATACAACC-----TAAAGAGGAAGTTCA	2089
Db	2884	AGAATTGCCCCATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCAG	2943
Qy	2090	TGTCCCAGATGAGTTCTCCAAAGATAGGGGTGATGTTTCAAAGGTGCCCCGACTGCCTCC	2149
Db	2944	TTTCTCAGATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCC	3003
Qy	2150	AGATGTTTCTGCTTTGGATGCTCAAGCAGAGATAGGCAGCATAGAAAAACCCAAAGTTCT	2209
Db	3004	AGATGTTTCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCT	3063
Qy	2210	TGTGAAAGAAGCCGAGAGAAAACTTCCTTCTGATACAGAAAAAGAGCGAAGATCTCCATC	2269
Db	3064	TGTGAAAGAAGCTGAGAAAAAACTTCCTTCCGATACAGAAAAAGAGGACAGATCACCATC	3123
Qy	2270	TGCTATATTTTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGA	2329
Db	3124	TGCTATATTTTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTGTACTGGAGAGA	3183
Qy	2330	CATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCTTGTTCTGCTGCTCTCGCTGACAGT	2389
Db	3184	CATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCCTATTCTGCTGCTTTCATTGACAGT	3243
Qy	2390	ATTCAGCATTGTGAGTGTAACGGCTACATTGCCTTGGCCCTGCTCTCTGTGACTATCAG	2449
Db	3244	ATTCAGCATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAG	3303
Qy	2450	CTTTAGGATATATAAGGGTGTGATCCAGGCTATCCAGAAATCTGATGAAGGCCACCCATT	2509
Db	3304	CTTTAGGATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATT	3363

Qy	2510	CAGGGCATATTTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTTCAGAAGTACAGCAA	2569
Db	3364	CAGGGCATATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTTCAGAAGTACAGTAA	3423
Qy	2570	TTCTGCTCTTGGTCATGTAACTGCACAATAAAAGAACTCAGACGCCTCTTCTTAGTTGA	2629
Db	3424	TTCTGCTCTTGGTCATGTGAAGTGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGA	3483
Qy	2630	TGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGC	2689
Db	3484	TGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGC	3543
Qy	2690	CTTGTTCAATGGTCTGACACTACTAATTTTGGCTCTGATTTCACTCTTCAGTGTTCTCTGT	2749
Db	3544	CTTGTTTAAATGGTCTGACACTACTGATTTTGGCTCTCATTTCACCTTCAGTGTTCTCTGT	3603
Qy	2750	TATTTATGAACGGCATCAGGCGCAAATAGATCATTATCTGGGACTTGCAAATAAGAATGT	2809
Db	3604	TATTTATGAACGGCATCAGGCACAGATAGATCATTATCTAGGACTTGCAAATAAGAATGT	3663
Qy	2810	TAAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGAATG	2869
Db	3664	TAAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCTGAATG	3723
Qy	2870	AGAAAGCCTGAAAGAGTTAACAATAGAGGAGTTTATCTTTAAAGGGGATATTCATTTGAT	2929
Db	3724	AAAACGCCCAAATAATTA-----GTAGGAGTTCATCTTTAAAGGGGATATTCATTTGA-	3777
Qy	2930	TCCATTGGGGAGGGTCAGGGAAGAACAAGCCTTGACATTGCAGTGCAGTTTCACAGATC	2989
Db	3778	-----TTATACGGATC	3788
Qy	2990	TTTATTTTGTAGCAACGCAGTG-TCTGAGGAAAAATGACCTGTCTTGACTGCCCTGTGTTT	3048
Db	3789	TTTATTTTGTAGCCATGCACTGTTGTGAGGAAAAATTACCTGTCTTGACTGCCATGTGTTT	3848
Qy	3049	ATCATCTTAAGTATTGTAAGCTGCTATGTATGGATTAAATCGTAATCATATTTGTTTTT	3108
Db	3849	ATCATCTTAAGTATTGTAAGCTGCTATGTATGGATTAAACCGTAATCATA--TCTTTTT	3906
Qy	3109	CCTGTATGAGGCACTGGTGAATAAACAAAGATCTGAGAAAGCTGTATATTACACTTTGTC	3168
Db	3907	CCTATCTGAGGCACTGGTGGA-----ATAAAAAACCTGTATATTTTACTTTGTT	3955
Qy	3169	GCAGGTAGTCTTGCTGTAT-TTGGGGAATTGCAAAGAAAGTGGAGCT-----GACAG	3219
Db	3956	GCAGATAGTCTTGCCGCATCTTGGCAAGTTGCAGAGATGGTGGAGCTAGAAAAAAAAG	4015
Qy	3220	AAATAACCCCTTTTCACAGTTTGTGCACTGTGTACGGTCTGTGTAGGTTGATGCAGATTTT	3279
Db	4016	AAAAAAGCCCTTTTCAGTTTGTGCACTGTGTATGGTCCGTGTAGATTGATGCAGATTTT	4075
Qy	3280	CTGAAATGAAA-----TGTTTACGAGATCATGCCACCAAGGCAGGAGTGAAAAAGCTTG	3335
Db	4076	CTGAAATGAAATGTTTGTGTTTACGAGATCATACCGGTAAAGCAGGAATGACAAAGCTTG	4135
Qy	3336	CCTTTCCTGGTATGTTCTAGGTGTATTGTGAAATTTACTGTTGTATTAATTGCCAATATA	3395

Accession	Source	Position	Sequence	Length
Db		4136	-CTTTTCTGGTATGTTCTAGGTGTATTGTGACTTTTACTGTTATATTAATTGCCAATATA	4194
Qy		3396	AGTAAATATAGATTATATATATCTATATATAGTGTTCACGAAGCTTAGCCCTTTACCTT	3455
Db		4195	AGTAAATATAGATTATA-----TATGTATAGTGTTCACAAAGCTTAGACCTTTACCTT	4248
Qy		3456	CCCAGCTGCCCCACAGTGCTTGATACT-----TCTGTGCATGGGTTTTATGTGTGTAGTC	3509
Db		4249	-CCAGCCACCCACAGTGCTTGATATTTCAGAGTCAGTCATTGGTTATACATGTGTAGTT	4307
Qy		3510	CCAAAGCACATAAGCTAGGGAGAAACGTACTTCTAGGCGCACTACCATCTGTTTTCAACA	3569
Db		4308	CCAAAGCACATAAGCTAGAAGAAGAAATATTCTAGGAGCACTACCATCTGTTTTCAACA	4367
Qy		3570	CGAACCGACGCCATGCAAACAGAACTCC-TCAACATAAACTTCACTGCACAGACTTACTG	3628
Db		4368	TGAA---ATGCCACACACATAGAACTCCAACAACATCAATTTTCATTGCACAGACTGACTG	4424
Qy		3629	TAGTTAATTTTATCAC--AAACTCTGGACTGAATCTAATGCTTCCAAAAA-----TGT	3679
Db		4425	TAGTTAATTTTGTACAGAATCTATGGACTGAATCTAATGCTTCCAAAAATGTTGTTTGT	4484
Qy		3680	TTGCAAATATCAAACATTGTTATGTAAGAAAATAT-----AAATGACGATTTATACA	3731
Db		4485	TTGCAAATATCAAACATTGTTATGCAAGAAATTATTAATTACAAAATGAAGATTTATACC	4544
Qy		3732	ATTGTGGTTTAAAGCTGTATTGA	3753
Db		4545	ATTGTGGTTTAAAGCTGTACTGA	4566

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FT          /product= "Nogo protein"
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XX
PN WO200151520-A2.
XX
PD 19-JUL-2001.
XX
PF 12-JAN-2001; 2001WO-US001041.
XX
PR 12-JAN-2000; 2000US-0175707P.
PR 26-MAY-2000; 2000US-0207366P.
PR 29-SEP-2000; 2000US-0236378P.
XX
PA (UYYA ) UNIV YALE.
XX
PI Strittmatter SM;
XX
DR WPI; 2001-442138/47.
DR P-PSDB; AAU09453.
XX
PT Novel Nogo receptor protein useful for identifying modulator of Nogo
PT protein or Nogo receptor protein, which is useful for treating central
PT nervous system disorders.
XX
PS Example 1; Page 95-100; 109pp; English.
XX
CC The sequence (Genbank accession number AB0202693) encodes the human Nogo
CC protein, a 250kDa myelin-associated axon growth inhibitor. The invention
CC relates to the use of the nogo receptor, nogo protein, their nucleic
CC acids, vectors expressing them and antibodies against them, to isolate
CC agents which block nogo receptor mediated axonal growth. The agent is
CC useful for treating a central nervous system disorder which is a result
CC of cranial or cerebral trauma, spinal cord injury, stroke or a
CC demyelinating disease selected from multiple sclerosis, monophasis
CC demyelination, encephalomyelitis, multifocal leukoencephalopathy,
CC panencephalitis, Marchiafava-Bignami disease, pontine myelinolysis,
CC adrenoleukodystrophy, Pelizaeus-Merzbacher disease, Spongy degeneration,
CC Alexander's disease, Canavan's disease, metachromatic leukodystrophy,
CC viral infection and Krabbe's disease
XX
SQ Sequence 4053 BP; 1189 A; 922 C; 922 G; 1020 T; 0 U; 0 Other;

Query Match          62.1%; Score 2379.4; DB 4; Length 4053;
Best Local Similarity 86.6%; Pred. No. 0;
Matches 2802; Conservative 0; Mismatches 381; Indels 54; Gaps 14;

Qy      1 CTATCTCCTCTCTCAGCCGCTGCTTTTAAAGAACGTGAATACCTTGGTGATTTACCAGCA 60
      || |||||
Db      846 CTGTCTCCTCTCTCAGCCGCTTCTTTCAAAGAACATGAATACCTTGGTAATTTGTCAACA 905

Qy      61 GTACTGCCCCACTGAAGGAACACTTCCAGCAACTTCAAATGAAGCTTCTAAAGCATTCTCA 120
      ||| | |||||
Db      906 GTATTACCCACTGAAGGAACACTTCAAGAAAATGTCAGTGAAGCTTCTAAAGAGGTCTCA 965

Qy      121 GAGAAGGCCAAAAAATCCATTTGTAGAGAGAAATTTAACAGAATTTTCAGAATTGGAATAT 180
      |||||
Db      966 GAGAAGGCCAAAACTCTACTCATAGATAGAGATTTAACAGAGTTTTTCAGAATTAGAATAC 1025

Qy      181 TCAGAAATGGAATCATCATTCAGTGGCTCTCAAAAGGCAGAACCTGCCGTAACAGTAGCG 240

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Db	1026	TCAGAAATGGGATCATCGTTTCAGTGTCTCTCCAAAAGCAGAATCTGCCGTAATAGTAGCA	1085
Qy	241	AATCCTAGGGACGAAATAGTTGTGAGGAGTAGAGATAAAGAAGAGGACTTAGTTAGTCTT	300
Db	1086	AATCCTAGGGAAGAAATAATCGTGAAAAATAAAGATGAAGAAGAGAAGTTAGTTAGTAAT	1145
Qy	301	AACATCCTTCATACTCAGCAGGAGTTATCTACAGTCCTTACGAAATCAGTTGAAGAAGAA	360
Db	1146	AACATCCTTCATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGGTTAAAGAGGAT	1205
Qy	361	GATAGAGTTCTGTCTCCAGAAAAACAAAGGACAGTTTTTAAGGAAAAGGGAGTTGCAGCA	420
Db	1206	GA---AGTTGTGTCTTCAGAAAAAGCAAAGACAGTTTTTAATGAAAAGAGAGTTGCAGTG	1262
Qy	421	GAAGCTTCTATGGGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTG	480
Db	1263	GAAGCTCCTATGAGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTG	1322
Qy	481	AAAGATACTTACAAGCAAGATAGTGATGTTTTGATTGCTGGAGGTAATATAGAGAGCAAA	540
Db	1323	AAAGATAGT---AAGGAAGATAGTGATATGTTGGCTGCTGGAGGTAATAATCGAGAGCAAC	1379
Qy	541	TTGGAAGGTAAAGTGGATAAGAAACACTTTTCAGATAGCCTTGAACAAACAAATCGTGAA	600
Db	1380	TTGGAAGGTAAAGTGGATAAAAAATGTTTTGCAGATAGCCTTGAACAAACTAATCACGAA	1439
Qy	601	AAAGATAGTGAAAGCAGTAATGATGACACTTCATTTCCCAGTACACCAGAAGCTGTAAGA	660
Db	1440	AAAGATAGTGAGAGTAGTAATGATGATACTTCTTTCCCAGTACGCCAGAAGGTATAAAG	1499
Qy	661	GGTGGTTCCGGAGCGTACATCACGTGTGCTCCCTTTAACC---CAACAACCTGAGAATGTT	717
Db	1500	GATCGTTCAGGAGCATATATCACATGTGCTCCCTTTAACCCAGCAGCAACTGAGAGCATT	1559
Qy	718	TCAACAAACATTTTTCCCTTGTTGGAAGATCATACTTCGGAAAATAAGACAGATGAAAAA	777
Db	1560	GCAACAAACATTTTTCTTTGTTAGGAGATCCTACTTCAGAAAATAAGACCGATGAAAAA	1619
Qy	778	AAGATAGAA-AAAAAAGGCACAAATTGTAACAGAGAAGAATGCAAGTGTCAAGACATCA	836
Db	1620	AAAATAGAAGAAAAGAAGGCCCAAATAGTAACAGAGAAGAATACTAGCACCAAAACATCA	1679
Qy	837	AACCCCTTTCCTTATGGCAGCACAGGAGTCTAAGACAGATTACGTTACAACAGATCATGTG	896
Db	1680	AACCCCTTTCTTGTAGCAGCACAGGATTCTGAGACAGATTATGTCACAACAGATAATTTA	1739
Qy	897	TCAAAGGTGACCGAGGAAGTAGTGGCAAACATGCCTGAAGGTCTAACCCAGATTTGGTT	956
Db	1740	ACAAAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCCAGATTTAGTA	1799
Qy	957	CAGGAAGCATGTGAAAGTGAATTGAATGAAGCTACTGGTACAAAAATTGCCTTTGAAACA	1016
Db	1800	CAGGAAGCATGTGAAAGTGAATTGAATGAAGTTACTGGTACAAAGATTGCTTATGAAACA	1859
Qy	1017	AAAATGGACCTGGTTCAAACCTTCAGAAGCTGTGCAGGAGTCACTTTACCCTGTAACACAG	1076

Db	1860	AAAATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCACAG	1919
Qy	1077	CTTTGCCCATCTTTTGAAGAATCTGAAGCTACTCCGTCACCGGTTTTGCCTGACATTGTC	1136
Db	1920	CTTTGCCCATCATTGAAGAGTCAGAAGCTACTCCTTCACCAGTTTTGCCTGACATTGTT	1979
Qy	1137	ATGGAAGCACCATTAAATTCTGTAGTTCCTAGTGCTGGTGCTTCTGCAGTGCAGCTCAGT	1196
Db	1980	ATGGAAGCACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGATACAGCCCAGC	2039
Qy	1197	TCATCACCATTAGAAACTCTTCCTTCAGTTAATTATGAAAGCATAAAGTTTGAGCCTGAA	1256
Db	2040	TCATCACCATTAGAAGC---TTCTTCAGTTAATTATGAAAGCATAAACATGAGCCTGAA	2096
Qy	1257	AATCCCCCACCATATGAGGAGGCCATGAATGTATCACTAAAAAAGAATCAGGAATGAAT	1316
Db	2097	AACCCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAGTATCAGGAATAAAG	2156
Qy	1317	GAAGAAATCACAGAGCCTGAAGGTATTAGTGTAGCTGTTTCAGGAAACAGAAGCTCCTTAT	1376
Db	2157	GAAGAAATTAAAGAGCCTGAAATATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTAT	2216
Qy	1377	ATATCTATTGCATGTGATTTAATTAAAGAAACAAAGATCTCTACTGAACCGACTCCAGAT	1436
Db	2217	ATATCTATTGCATGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAACCAGCTCCGGAT	2276
Qy	1437	TTCTCTAGTTATTCAGAAATAGCAGAAGTTGCACAGCCAGTGCCCCGAGCATTCTGAGCTA	1496
Db	2277	TTCTCTGATTATTCAGAAATGGCAAAAGTTGAACAGCCAGTGCCCTGATCATTCTGAGCTA	2336
Qy	1497	GTTGAAGATTCCTCCCCGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCC	1556
Db	2337	GTTGAAGATTCCTCACCTGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCT	2396
Qy	1557	GAAGTTCCACAAAAACAAGATGAAGCTGTAATACTTGTGAAAGAAAACCTCACTGAAATT	1616
Db	2397	GACGTTCCACAAAAACAAGATGAAACTGTGATGCTTGTGAAAGAAAGTCTCACTGAGACT	2456
Qy	1617	TCATCTGAGTCAATGACAGGACATGACAATAAGGGAAAACTCAGTGCTTCACCATCACCT	1676
Db	2457	TCATTTGAGTCAATGATAGAATATGAAAATAAGGAAAAACTCAGTGCTTTGC---CACCT	2513
Qy	1677	GAGGGAGGAAAACCGTATTTGGAGTCTTTTCAGCCCAGTTTAGGCATCACAAAAGATACC	1736
Db	2514	GAGGGAGGAAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATACC	2573
Qy	1737	TTAGCACCTGATGAAGTTTCAGCATTGACCCAAAAGGAGAAAATCCCTTTGCAGATGGAG	1796
Db	2574	CTGTTACCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAATTCCTTTGCAGATGGAG	2633
Qy	1797	GAGCTCAATACTGCAGTTTATTCAAGTGATGGCTTATTCATTGCTCAGGAAGCAAACCTA	1856
Db	2634	GAGCTCAGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGATA	2693
Qy	1857	AGAGAAAAGTGAAACATTTTCAGATTCATCTCCGATTGAGATTATAGATGAGTCCCGACC	1916
Db	2694	AGAGAAACTGAAACGTTTTCAGATTCATCTCCAATTGAAATTATAGATGAGTCCCTACA	2753

Qy	1917	TTTGT CAGTTCTAAAGCAGATTCTTCTCCTACATTAGCCAGGGAATACACTGACCTAGAA	1976
Db	2754	TTGATCAGTTCTAAACTGATTCATTTTCTAAATTAGCCAGGGAATATACTGACCTAGAA	2813
Qy	1977	GTAGCCACAAAAGTGAAATTGCTGACATCCAGGATGGAGCTGGGTTCATTGGCTTGTGCA	2036
Db	2814	GTATCCACAAAAGTGAAATTGCTAATGCCCCGGATGGAGCTGGGTTCATTGCCTTGCACA	2873
Qy	2037	GGATTGCCCCATGACCTTTTCTTTCAAGAGTATACAACC-----TAAAGAGGAAGTTCAT	2090
Db	2874	GAATTGCCCCATGACCTTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCAGT	2933
Qy	2091	GTCCCAGATGAGTTCTCCAAAGATAGGGGTGATGTTTCAAAGGTGCCCGTACTGCCTCCA	2150
Db	2934	TTCTCAGATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCA	2993
Qy	2151	GATGTTTCTGCTTTGGATGCTCAAGCAGAGATAGGCAGCATAGAAAAACCCAAAGTTCTT	2210
Db	2994	GATGTTTCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTT	3053
Qy	2211	GTGAAAGAAGCCGAGAGAAAACCTTCCTTCTGATACAGAAAAAGAGCGAAGATCTCCATCT	2270
Db	3054	GTGAAAGAAGCTGAGAAAAAACTTCCTTCCGATACAGAAAAAGAGGACAGATCACCATCT	3113
Qy	2271	GCTATATTTTTCAGCAGAGCTGAGTAAAACCTCAGTTGTTGACCTCCTCTACTGGAGAGAC	2330
Db	3114	GCTATATTTTTCAGCAGAGCTGAGTAAAACCTCAGTTGTTGACCTCCTGTACTGGAGAGAC	3173
Qy	2331	ATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCTTGTTCTGCTGCTCTCGCTGACAGTA	2390
Db	3174	ATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCCTATTCTGCTGCTTTTCATTGACAGTA	3233
Qy	2391	TTCAGCATTGTGAGTGTAACGGCCTACATTGCCTTGCCCTGCTCTCTGTGACTATCAGC	2450
Db	3234	TTCAGCATTGTGAGCGTAACAGCCTACATTGCCTTGCCCTGCTCTCTGTGACCATCAGC	3293
Qy	2451	TTTAGGATATATAAGGGTGTGATCCAGGCTATCCAGAAATCTGATGAAGGCCACCCATTC	2510
Db	3294	TTTAGGATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTC	3353
Qy	2511	AGGGCATATTTGGAATCTGAAGTTGCTATATCTGAGGAGTTGTTTCAGAAGTACAGCAAT	2570
Db	3354	AGGGCATATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGTTTCAGAAGTACAGTAAT	3413
Qy	2571	TCTGCTCTTGGTCATGTTAAGTGCACAATAAAAGAACTCAGACGCCTCTTCTTAGTTGAT	2630
Db	3414	TCTGCTCTTGGTCATGTGAAGTGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGAT	3473
Qy	2631	GATTTAGTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCC	2690
Db	3474	GATTTAGTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCC	3533
Qy	2691	TTGTTCAATGGTCTGACACTACTAATTTTGGCTCTGATTTCACTCTTCAGTGTTTCTGTT	2750
Db	3534	TTGTTTAAATGGTCTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTTTCTGTT	3593

Qy	2751	ATTTATGAACGGCATCAGGCGCAAATAGATCATTATCTGGGACTTGCAAATAAGAATGTT	2810
Db	3594	ATTTATGAACGGCATCAGGCACAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTT	3653
Qy	2811	AAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGAATGA	2870
Db	3654	AAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCTGAATGA	3713
Qy	2871	GAAAGCCTGAAAGAGTTAACAATAGAGGAGTTTATCTTTAAAGGGGATATTCATTTGATT	2930
Db	3714	AAACGCCCAAAATAATTA-----GTAGGAGTTCATCTTTAAAGGGGATATTCATTTGATT	3768
Qy	2931	CCATTGGGGAGGGTCAGGGAAGAACAAGCCTTGACATTGCAGTGCAGTTTCAC-----	2984
Db	3769	ATACGGGGGAGGGTCAGGGAAGAACGAA-CCTTGACGTTGCAGTGCAGTTTCACAGATCG	3827
Qy	2985	-----AGATCTTTATTTTGTAGCAACGCAGTG-TCTGAGGAAAAATGACCTGTCTTGACTG	3038
Db	3828	TTGTTAGATCTTTATTTTGTAGCCATGCACTGTTGTGAGGAAAAATTACCTGTCTTGACTG	3887
Qy	3039	CCCTGTGTTTCATCATCTTAAGTATTGTAAGCTGCTATGTATGGATTTAAATCGTAATCAT	3098
Db	3888	CCATGTGTTTCATCATCTTAAGTATTGTAAGCTGCTATGTATGGATTTAAACCGTAATCAT	3947
Qy	3099	ATTTGTTTTTCCTGTATGAGGCACTGGTGAATAAACAAAGATCTGAGAAAGCTGTATATT	3158
Db	3948	A--TCTTTTTCCTATCTGAGGCACTGGTGGA-----ATAAAAAACCTGTATATT	3994
Qy	3159	ACACTTTGTGCGCAGGTAGTCTTGCTGTAT-TTGGGGAATTGCAAAGAAAGTGGAGCT	3214
Db	3995	TTACTTTGTTGCAGATAGTCTTGCCGCATCTGGCAAGTTGCAGAGATGGTGGAGCT	4051

RESULT 6

ACC81048

ID ACC81048 standard; cDNA; 4053 BP.

XX

AC ACC81048;

XX

DT 22-JUL-2003 (first entry)

XX

DE Human NogoA gene.

XX

KW Human; Nogo receptor; NgR; CTS domain; neuroprotective; gene therapy;
KW axonal growth; central nervous system; CNS; Nogo; spinal cord injury;
KW cranial trauma; cerebral trauma; spinal trauma; stroke; Krabbe's disease;
KW demyelinating disease; multiple sclerosis; monophasic demyelination;
KW encephalomyelitis; multifocal leukoencephalopathy; panencephalitis; gene;
KW ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 135..3713

FT /*tag= a

FT /product= "Human NogoA"

XX

Db	966	GAGAAGGCCAAAACTCTACTCATAGATAGAGATTTTAACAGAGTTTTCAGAATTAGAATAC	1025
Qy	181	TCAGAAATGGAATCATCATTCACTGGCTCTCAAAAGGCAGAACCTGCCGTAACAGTAGCG	240
Db	1026	TCAGAAATGGGATCATCGTTCAGTGTCTCTCCAAAAGCAGAATCTGCCGTAATAGTAGCA	1085
Qy	241	AATCCTAGGGACGAAATAGTTGTGAGGAGTAGAGATAAAGAAGAGGACTTAGTTAGTCTT	300
Db	1086	AATCCTAGGGAAGAAATAATCGTGAAAAATAAAGATGAAGAAGAGAAGTTAGTTAGTAAT	1145
Qy	301	AACATCCTTCATACTCAGCAGGAGTTATCTACAGTCCTTACGAAATCAGTTGAAGAAGAA	360
Db	1146	AACATCCTTCATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGGTTAAAGAGGAT	1205
Qy	361	GATAGAGTTCTGTCTCCAGAAAAAACAAAGGACAGTTTTTAAGGAAAAGGGAGTTGCAGCA	420
Db	1206	GA---AGTTGTGTCTTCAGAAAAAGCAAAGACAGTTTTAATGAAAAGAGAGTTGCAGTG	1262
Qy	421	GAAGCTTCTATGGGGGAGGAATATGCAGACTTCAAACCATTGAGCGAGTATGGGAAGTG	480
Db	1263	GAAGCTCCTATGAGGGAGGAATATGCAGACTTCAAACCATTGAGCGAGTATGGGAAGTG	1322
Qy	481	AAAGATACTTACAAGCAAGATAGTGATGTTTTGATTGCTGGAGGTAATATAGAGAGCAAA	540
Db	1323	AAAGATAGT---AAGGAAGATAGTGATATGTTGGCTGCTGGAGGTAATATCGAGAGCAAC	1379
Qy	541	TTGGAAGGTAAAGTGGATAAGAAACACTTTTCAGATAGCCTTGAACAAACAAATCGTGAA	600
Db	1380	TTGGAAAGTAAAGTGGATAAAAAAATGTTTTGCAGATAGCCTTGAACAAACTAATCACGAA	1439
Qy	601	AAAGATAGTGAAAGCAGTAATGATGACACTTCATTTCCAGTACACCAGAAGCTGTAAGA	660
Db	1440	AAAGATAGTGAGAGTAGTAATGATGATACTTCTTTCCAGTACGCCAGAAGGTATAAAG	1499
Qy	661	GGTGGTTCCGGAGCGTACATCACGTGTGCTCCCTTTAACC---CAACAACGAGAATGTT	717
Db	1500	GATCGTTCCAGGAGCATATATCACATGTGCTCCCTTTAACCAGCAGCAACTGAGAGCATT	1559
Qy	718	TCAACAAACATTTTTCCCTTGTTGGAAGATCATACTTCGGAAAATAAGACAGATGAAAAA	777
Db	1560	GCAACAAACATTTTTCTTTGTTAGGAGATCCTACTTCAGAAAATAAGACCGATGAAAAA	1619
Qy	778	AAGATAGAA-AAAAAAGGCACAAATTGTAACAGAGAAGAATGCAAGTGTCAAGACATCA	836
Db	1620	AAAATAGAAGAAAAGAAGGCCCAAATAGTAACAGAGAAGAATACTAGCACCAAACATCA	1679
Qy	837	AACCCTTTCCTTATGGCAGCACAGGAGTCTAAGACAGATTACGTTACAACAGATCATGTG	896
Db	1680	AACCCTTTCCTTGTAGCAGCACAGGATTCTGAGACAGATTATGTCACAACAGATAATTTA	1739
Qy	897	TCAAAGGTGACCGAGGAAGTAGTGGCAAACATGCCTGAAGGTCTAACCCAGATTTGGTT	956
Db	1740	ACAAAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCCAGATTTAGTA	1799
Qy	957	CAGGAAGCATGTGAAAGTGAATTGAATGAAGCTACTGGTACAAAAATTGCCTTTGAAACA	1016
Db	1800	CAGGAAGCATGTGAAAGTGAATTGAATGAAGTTACTGGTACAAAGATTGCTTATGAAACA	1859

Qy	1017	AAAATGGACCTGGTTCAAACCTCAGAAGCTGTGCAGGAGTCACTTTACCCTGTAACACAG	1076
Db	1860	AAAATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCACAG	1919
Qy	1077	CTTTGCCCATCTTTGAAGAATCTGAAGCTACTCCGTCACCGGTTTTGCCTGACATTGTC	1136
Db	1920	CTTTGCCCATCATTTGAAGAGTCAGAAGCTACTCCTTCACCAGTTTTGCCTGACATTGTT	1979
Qy	1137	ATGGAAGCACCATTAAATTCTGTAGTTCCTAGTGCTGGTGCTTCTGCAGTGCAGCTCAGT	1196
Db	1980	ATGGAAGCACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGATACAGCCCAGC	2039
Qy	1197	TCATCACCATTAGAACTCTTCCTTCAGTTAATTATGAAAGCATAAAGTTTGAGCCTGAA	1256
Db	2040	TCATCACCATTAGAAGC---TTCTTCAGTTAATTATGAAAGCATAAACATGAGCCTGAA	2096
Qy	1257	AATCCCCCACCATATGAGGAGGCCATGAATGTATCACTAAAAAAGAATCAGGAATGAAT	1316
Db	2097	AACCCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAGTATCAGGAATAAAG	2156
Qy	1317	GAAGAAATCACAGAGCCTGAAGGTATTAGTGTAGCTGTTTCAGGAAACAGAAGCTCCTTAT	1376
Db	2157	GAAGAAATTAAAGAGCCTGAAAATATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTAT	2216
Qy	1377	ATATCTATTGCATGTGATTTAATTAAAGAAACAAAGATCTCTACTGAACCGACTCCAGAT	1436
Db	2217	ATATCTATTGCATGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAACCAGCTCCGGAT	2276
Qy	1437	TTCTCTAGTTATTTCAGAAATAGCAGAAGTTGCACAGCCAGTGCCCCGAGCATTCTGAGCTA	1496
Db	2277	TTCTCTGATTATTTCAGAAATGGCAAAAGTTGAACAGCCAGTGCCCTGATCATTCTGAGCTA	2336
Qy	1497	GTTGAAGATTCCCTCCCCGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCC	1556
Db	2337	GTTGAAGATTCCCTCACCTGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCT	2396
Qy	1557	GAAGTTCCACAAAAACAAGATGAAGCTGTAATACTTGTGAAAGAAAACCTCACTGAAATT	1616
Db	2397	GACGTTCCACAAAAACAAGATGAACTGTGATGCTTGTGAAAGAAAGTCTCACTGAGACT	2456
Qy	1617	TCATCTGAGTCAATGACAGGACATGACAATAAGGGAAACTCAGTGCTTCACCATCACCT	1676
Db	2457	TCATTTGAGTCAATGATAGAATATGAAAATAAGGAAAACTCAGTGCTTTGC---CACCT	2513
Qy	1677	GAGGGAGGAAAACCGTATTTGGAGTCTTTTCAGCCAGTTTAGGCATCACAAAAGATACC	1736
Db	2514	GAGGGAGGAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATACC	2573
Qy	1737	TTAGCACCTGATGAAGTTTCAGCATTGACCCAAAAGGAGAAAATCCCTTTGCAGATGGAG	1796
Db	2574	CTGTTACCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAATTCCTTTGCAGATGGAG	2633
Qy	1797	GAGCTCAATACTGCAGTTTATTCAAAGTGATGGCTTATTCATTGCTCAGGAAGCAAACCTA	1856
Db	2634	GAGCTCAGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGATA	2693

Qy	1857	AGAGAAAGTGAAACATTTTCAGATTTCATCTCCGATTGAGATTATAGATGAGTTCCCGACC	1916
Db	2694	AGAGAAACTGAAACGTTTTTCAGATTTCATCTCCAATTGAAATTATAGATGAGTTCCCTACA	2753
Qy	1917	TTTGTCTAGTTCTAAAGCAGATTCTTCTCCTACATTAGCCAGGGAATACACTGACCTAGAA	1976
Db	2754	TTGATCAGTTCTAAACTGATTTCATTTTCTAAATTAGCCAGGGAATATACTGACCTAGAA	2813
Qy	1977	GTAGCCACAAAAGTGAAATTGCTGACATCCAGGATGGAGCTGGGTCATTGGCTTGTGCA	2036
Db	2814	GTATCCACAAAAGTGAAATTGCTAATGCCCCGGATGGAGCTGGGTCATTGCCTTGCACA	2873
Qy	2037	GGATTGCCCCATGACCTTTCTTTCAAGAGTATACAACC-----TAAAGAGGAAGTTCAT	2090
Db	2874	GAATTGCCCCATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCAGT	2933
Qy	2091	GTCCCGATGAGTTCTCCAAAGATAGGGGTGATGTTTCAAAGGTGCCCGTACTGCCTCCA	2150
Db	2934	TTCTCAGATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCA	2993
Qy	2151	GATGTTTCTGCTTTGGATGCTCAAGCAGAGATAGGCAGCATAGAAAAACCCAAAGTTCTT	2210
Db	2994	GATGTTTCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTT	3053
Qy	2211	GTGAAAGAAGCCGAGAGAAAACCTTCCTTCTGATACAGAAAAAGAGCGAAGATCTCCATCT	2270
Db	3054	GTGAAAGAAGCTGAGAAAAACCTTCCTTCCGATACAGAAAAAGAGGACAGATCACCATCT	3113
Qy	2271	GCTATATTTTCAGCAGAGCTGAGTAAAACCTTCAGTTGTTGACCTCCTCTACTGGAGAGAC	2330
Db	3114	GCTATATTTTCAGCAGAGCTGAGTAAAACCTTCAGTTGTTGACCTCCTGTACTGGAGAGAC	3173
Qy	2331	ATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCTTGTTTCCTGCTGCTCTCGCTGACAGTA	2390
Db	3174	ATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCCTATTTCCTGCTGCTTTTCATTGACAGTA	3233
Qy	2391	TTCAGCATTGTGAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCTGTGACTATCAGC	2450
Db	3234	TTCAGCATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGC	3293
Qy	2451	TTTAGGATATATAAGGGTGTGATCCAGGCTATCCAGAAATCTGATGAAGGCCACCCATTC	2510
Db	3294	TTTAGGATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTC	3353
Qy	2511	AGGGCATATTTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGCAAT	2570
Db	3354	AGGGCATATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGTAAT	3413
Qy	2571	TCTGCTCTTGGTCATGTTAACTGCACAATAAAAGAACTCAGACGCCTCTTCTTAGTTGAT	2630
Db	3414	TCTGCTCTTGGTCATGTGAACCTGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGAT	3473
Qy	2631	GATTTAGTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCC	2690
Db	3474	GATTTAGTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCC	3533
Qy	2691	TTGTTCAATGGTCTGACACTACTAATTTTGGCTCTGATTTCACTCTTCAGTGTTTCCTGTT	2750

FT CDS 1048. .3729
 FT /*tag= a
 FT /product= "Human secreted protein vb22_1"
 XX
 PN WO200011015-A1.
 XX
 PD 02-MAR-2000.
 XX
 PF 24-AUG-1999; 99WO-US019351.
 XX
 PR 24-AUG-1998; 98US-0097638P.
 PR 24-AUG-1998; 98US-0097659P.
 PR 09-SEP-1998; 98US-0099618P.
 PR 28-SEP-1998; 98US-0102092P.
 PR 25-NOV-1998; 98US-0109978P.
 PR 23-DEC-1998; 98US-0113645P.
 PR 23-DEC-1998; 98US-0113646P.
 PR 23-AUG-1999; 99US-00379246.
 XX
 PA (ALPH-) ALPHAGENE INC.
 XX
 PI Valenzuela D, Yuan O, Hoffman H, Hall J, Rapiejko P;
 XX
 DR WPI; 2000-224657/19.
 DR P-PSDB; AAY95012, AAY95030.
 XX
 PT New secreted or transmembrane proteins and polynucleotides encoding them,
 PT useful for treating neurodegenerative disorders, autoimmune diseases and
 PT cancer.
 XX
 PS Claim 72; Page 321-322; 357pp; English.
 XX
 CC The invention relates to 40 human secreted proteins (AAY94981-Y95020),
 CC and cDNA sequences encoding them (AAA23423-A23462). The secreted proteins
 CC of the invention include those that are thought to be only partially
 CC secreted, i.e., transmembrane proteins. The proteins of the invention may
 CC exhibit one or more activities selected from the following: cytokine
 CC activity; cell proliferation; differentiation; immune modulation;
 CC haematopoiesis regulation; tissue growth activity; activin/inhibin
 CC activity; chemotactic/chemokinetic activity; haemostatic and thrombolytic
 CC activity; anti-inflammatory activity; and tumour inhibition activity. The
 CC proteins may be administered to patients as vaccines, and the nucleotides
 CC may be used as part of a gene therapy regime. Diseases or conditions that
 CC may be treated using the proteins or nucleotides of the invention include
 CC autoimmune diseases; genetic disorders; haemophilia; cardiovascular
 CC diseases; cancer; bacterial, fungal and viral infections, especially HIV;
 CC multiple sclerosis; rheumatoid arthritis; pulmonary inflammation;
 CC Guillain-Barre syndrome; insulin dependent diabetes mellitus; and
 CC allergic reactions such as asthma and anaemia. They may also be used for
 CC treating wounds, burns, ulcers, osteoporosis, osteoarthritis, periodontal
 CC diseases, Alzheimer's disease, Parkinson's disease, Huntington's disease
 CC and amyotrophic lateral sclerosis (ALS). Proteins with activin/inhibin
 CC activity may additionally be useful as contraceptives. Nucleic acid
 CC sequences of the invention may be used in chromosome mapping, and as a
 CC source of diagnostic primers and probes. The present sequence represents
 CC cDNA encoding one of the 40 proteins of the invention
 XX

SQ Sequence 4093 BP; 1213 A; 926 C; 928 G; 1026 T; 0 U; 0 Other;

Query Match 61.8%; Score 2370.4; DB 3; Length 4093;
Best Local Similarity 86.4%; Pred. No. 0;
Matches 2807; Conservative 0; Mismatches 386; Indels 55; Gaps 15;

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Qy      1 CTATCTCCTCTCTCAGCCGCTGCTTTTAAAGAACGTGAATACCTTGGTGATTACCAGCA 60
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Db      863 CTGTCTCCTCTCTCAGCCGCTTCTTTCAAAGAACATGAATACCTTGGTAATTTGTCAACA 922

Qy      61 GTACTGCCCCACTGAAGGAACACTTCCAGCAACTTCAAATGAAGCTTCTAAAGCATTCTCA 120
      ||| | |||||
Db      923 GTATTACCCACTGAAGGAACACTTCAAGAAAATGTCAGTGAAGCTTCTAAAGAGGTCTCA 982

Qy     121 GAGAAGGCAAAAAATCCATTTGTAGAGAGAAATTTAACAGAATTTTCAGAATTGGAATAT 180
      ||||| ||| || | ||| ||| |||||
Db     983 GAGAAGGC-AAAACTCTACTCATAGATAGAGATTTAACAGAGTTTTCAGAATTAGAATAC 1041

Qy     181 TCAGAAATGGAATCATCATTCAGTGGCTCTCAAAAGGCAGAACCTGCCGTAACAGTAGCG 240
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Db    1042 TCAGAAATGGGATCATCGTTTCAGTGTCTCTCCAAAAGCAGAACTCTGCCGTAATAGTAGCA 1101

Qy     241 AATCCTAGGGACGAAATAGTTGTGAGGAGTAGAGATAAAGAAGAGGACTTAGTTAGTCTT 300
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Db    1102 AATCCTAGGGAAGAAATAATCGTGAAAAATAAAGATGAAGAAGAGAAGTTAGTTAGTAAT 1161

Qy     301 AACATCCTTCATACTCAGCAGGAGTTATCTACAGTCCTTACGAAATCAGTTGAAGAAGAA 360
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Db    1162 AACATCCTTCATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGGTTAAAGAGGAT 1221

Qy     361 GATAGAGTTCTGTCTCCAGAAAAACAAAGGACAGTTTTAAGGAAAAGGGAGTTGCAGCA 420
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Db    1222 GA---AGTTGTGTCTTCAGAAAAAGCAAAGACAGTTTTAATGAAAAGAGAGTTGCAGTG 1278

Qy     421 GAAGCTTCTATGGGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTG 480
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Db    1279 GAAGCTCCTATGAGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTG 1338

Qy     481 AAAGATACTTACAAGCAAGATAGTGATGTTTTGATTGCTGGAGGTAATATAGAGAGCAAA 540
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Db    1339 AAAGATAGT---AAGGAAGATAGTGATATGTTGGCTGCTGGAGGTAATATCGAGAGCAAC 1395

Qy     541 TTGGAAGGTAAAGTGGATAAGAAACACTTTTCAGATAGCCTTGAACAAACAATCGTGAA 600
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Db    1396 TTGGAAGGTAAAGTGGATAAAAAATGTTTTGCAGATAGCCTTGAACAACTAATCACGAA 1455

Qy     601 AAAGATAGTGAAAGCAGTAATGATGACACTTCATTTCCCAGTACACCAGAAGCTGTAAGA 660
      ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    1456 AAAGATAGTGAGAGTAGTAATGATGATACTTCTTTCCCAGTACGCCAGAAGGTATAAAG 1515

Qy     661 GGTGGTTCCGGAGCGTACATCACGTGTGCTCCCTTTAACC---CAACAAGTGAATGTT 717
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Db    1516 GATCGTTCAGGAGCATATATCACATGTGCTCCCTTTAACCCAGCAGCAACTGAGAGCATT 1575

Qy     718 TCAACAAACATTTTCCCTTGTTGGAAGATCATACTTCGGAAAATAAGACAGATGAAAAA 777
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Db    1576 GCAACAAACATTTTCCCTTGTTAGGAGATCCTACTTCAGAAAATAAGACCGATGAAAAA 1635
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Qy	778	AAGATAGAA-AAAAAAGGCACAAATTGTAACAGAGAAGAATGCAAGTGTCAAGACATCA	836
Db	1636	AAAAATAGAAGAAAAGAAGGCCCAAATAGTAACAGAGAAGAATACTAGCACCAAACATCA	1695
Qy	837	AACCCCTTTCCTTATGGCAGCACAGGAGTCTAAGACAGATTACGTTACAACAGATCATGTG	896
Db	1696	AACCCCTTTTCTTGTAGCAGCACAGGATTCTGAGACAGATTATGTCACAACAGATAATTTA	1755
Qy	897	TCAAAGGTGACCGAGGAAGTAGTGGCAAACATGCCTGAAGGTCTAACCCAGATTTGGTT	956
Db	1756	ACAAAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCCAGATTTAGTA	1815
Qy	957	CAGGAAGCATGTGAAAGTGAATTGAATGAAGCTACTGGTACAAAAATTGCCTTTGAAACA	1016
Db	1816	CAGGAAGCATGTGAAAGTGAATTGAATGAAGTTACTGGTACAAAGATTGCTTATGAAACA	1875
Qy	1017	AAAATGGACCTGGTTCAAACTTCAGAAGCTGTGCAGGAGTCACTTTACCCTGTAACACAG	1076
Db	1876	AAAATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCACAG	1935
Qy	1077	CTTTGCCCATCTTTTGAAGAATCTGAAGCTACTCCGTCACCGGTTTTGCCTGACATTGTC	1136
Db	1936	CTTTGCCCATCATTTGAAGAGTCAGAAGCTACTCCTTCACCAAGTTTTGCCTGACATTGTT	1995
Qy	1137	ATGGAAGCACCATTAAATTCTGTAGTTCCTAGTGCTGGTGCTTCTGCAGTGCAGCTCAGT	1196
Db	1996	ATGGAAGCACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGATACAGCCCAGC	2055
Qy	1197	TCATCACCATTAGAACTCTTCCTCAGTTAATTATGAAAGCATAAAGTTTGAGCCTGAA	1256
Db	2056	TCATCACCATTAGAAGCTT---CTTCAGTTAATTATGAAAGCATAAAACATGAGCCTGAA	2112
Qy	1257	AATCCCCCACCATATGAGGAGGCCATGAATGTATCACTAAAAAAGAATCAGGAATGAAT	1316
Db	2113	AACCCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAGTATCAGGAATAAAG	2172
Qy	1317	GAAGAAATCAGAGGCCTGAAGGTATTAGTGTAGCTGTTCAGGAAACAGAAGCTCCTTAT	1376
Db	2173	GAAGAAATTAAAGAGCCTGAAAATATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTAT	2232
Qy	1377	ATATCTATTGCATGTGATTTAATTAAAGAAACAAAGATCTCTACTGAACCGACTCCAGAT	1436
Db	2233	ATATCTATTGCATGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAACAGCTCCGGAT	2292
Qy	1437	TTCTCTAGTTATTCAGAAATAGCAGAAGTTGCACAGCCAGTGCCCCGAGCATTCTGAGCTA	1496
Db	2293	TTCTCTGATTATTCAGAAATGGCAAAAGTTGAACAGCCAGTGCCCTGATCATTCTGAGCTA	2352
Qy	1497	GTTGAAGATTCTCCCCCGATTCTGAACCAAGTTGACTTATTTAGTGATGATTCAATACCC	1556
Db	2353	GTTGAAGATTCTCACCTGATTCTGAACCAAGTTGACTTATTTAGTGATGATTCAATACCT	2412
Qy	1557	GAAGTTCCACAAAAACAAGATGAAGCTGTAATACTTGTGAAAGAAAACCTCACTGAAATT	1616
Db	2413	GACGTTCCACAAAAACAAGATGAACTGTGATGCTTGTGAAAGAAAAGTCTCACTGAGACT	2472

Qy	1617	TCATCTGAGTCAATGACAGGACATGACAATAAGGGGAAAACCTCAGTGCTTCACCATCACCT	1676
Db	2473	TCATTTGAGTCAATGATAGAATATGAAAATAAGGAAAAACCTCAGTGCTTTGC---CACCT	2529
Qy	1677	GAGGGAGGAAAACCGTATTTGGAGTCTTTTCAGCCCAGTTTAGGCATCACAAAAGATACC	1736
Db	2530	GAGGGAGGAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATACC	2589
Qy	1737	TTAGCACCTGATGAAGTTTCAGCATTGACCCAAAAGGAGAAAATCCCTTTGCAGATGGAG	1796
Db	2590	CTGTTACCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAATTCCTTTGCAGATGGAG	2649
Qy	1797	GAGCTCAATACTGCAGTTTATTCAAGTGATGGCTTATTCATTGCTCAGGAAGCAAACCTA	1856
Db	2650	GAGCTCAGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGATA	2709
Qy	1857	AGAGAAAAGTGAAACATTTTCAGATTTCATCTCCGATTGAGATTATAGATGAGTTCCCGACC	1916
Db	2710	AGAGAAAAGTGAAACGTTTTCAGATTTCATCTCCAATTGAAATTATAGATGAGTTCCCTACA	2769
Qy	1917	TTTGTGAGTTCTAAAGCAGATTCTTCTCCTACATTAGCCAGGGAATACACTGACCTAGAA	1976
Db	2770	TTGATCAGTTCTAAAGCAGTTTCTTCTAAATTAGCCAGGGAATATACTGACCTAGAA	2829
Qy	1977	GTAGCCACAAAAGTGAAATTGCTGACATCCAGGATGGAGCTGGGTCATTGGCTTGTGCA	2036
Db	2830	GTATCCACAAAAGTGAAATTGCTAATGCCCCGGATGGAGCTGGGTCATTGCCCTGCACA	2889
Qy	2037	GGATTGCCCCATGACCTTTCTTTCAAGAGTATACAACCTA-----AAGAGGAAGTTCAT	2090
Db	2890	GAATTGCCCCATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCAGT	2949
Qy	2091	GTCCCAGATGAGTTCTCCAAAGATAGGGGTGATGTTTCAAAGGTGCCCCGACTGCCTCCA	2150
Db	2950	TTCTCAGATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCA	3009
Qy	2151	GATGTTTCTGCTTTGGATGCTCAAGCAGAGATAGGCAGCATAGAAAAACCCAAAGTTCTT	2210
Db	3010	GATGTTTCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTT	3069
Qy	2211	GTGAAAGAAGCCGAGAGAAAACCTTCCTTCTGATACAGAAAAAGAGCGAAGATCTCCATCT	2270
Db	3070	GTGAAAGAAGCTGAGAAAAAACTTCCTTCCGATACAGAAAAAGAGACAGATCACCATCT	3129
Qy	2271	GCTATATTTTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGAC	2330
Db	3130	GCTATATTTTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTGTACTGGAGAGAC	3189
Qy	2331	ATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCTTGTTCCCTGCTGCTCTCGCTGACAGTA	2390
Db	3190	ATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCCTATTCCCTGCTGCTTTTCATTGACAGTA	3249
Qy	2391	TTCAGCATTGTGAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCTGTGACTATCAGC	2450
Db	3250	TTCAGCATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGC	3309
Qy	2451	TTTAGGATATATAAGGGTGTGATCCAGGCTATCCAGAAATCTGATGAAGGCCACCCATTC	2510

Db	3310	TTTAGGATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTC	3369
Qy	2511	AGGGCATATTTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGCAAT	2570
Db	3370	AGGGCATATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGTAAT	3429
Qy	2571	TCTGCTCTTGGTCATGTAACTGCACAATAAAAGAACTCAGACGCCTCTTCTTAGTTGAT	2630
Db	3430	TCTGCTCTTGGTCATGTGAACTGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGAT	3489
Qy	2631	GATTTAGTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCC	2690
Db	3490	GATTTAGTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCC	3549
Qy	2691	TTGTTCAATGGTCTGACACTACTAATTTTGGCTCTGATTTCACTCTTCAGTGTTCTGT	2750
Db	3550	TTGTTTAATGGTCTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTTCTGT	3609
Qy	2751	ATTTATGAACGGCATCAGGCGCAAATAGATCATTATCTGGGACTTGCAAATAAGAATGTT	2810
Db	3610	ATTTATGAACGGCATCAGGCACAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTT	3669
Qy	2811	AAAGATGCTATGGCTAAAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGAATGA	2870
Db	3670	AAAGATGCTATGGCTAAAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGAATGA	3729
Qy	2871	GAAAGCCTGAAAGAGTTAACAATAGAGGAGTTTATCTTTAAAGGGGATATTCATTTGATT	2930
Db	3730	AAACGCCCAAAATAATTA-----GTAGGAGTTCATCTTTAAAGGGGATATTCATTTGATT	3784
Qy	2931	CCATTGGGGAGGGTCAGGGAAGAACAAGCCTTGACATTGCAGTGCAGTTTCAC-----	2984
Db	3785	ATACGGGGGAGGGTCAGGGAAGAACGAA-CCTTGACGTTGCAGTGCAGTTTCACAGATCG	3843
Qy	2985	-----AGATCTTTATTTTTAGCAACGCAGTG-TCTGAGGAAAAATGACCTGTCTTGACTG	3038
Db	3844	TTGTTAGATCTTTATTTTTAGCCATGCACTGTTGTGAGGAAAAATTACCTGTCTTGACTG	3903
Qy	3039	CCCTGTGTTTCATCATCTTAAGTATTGTAAGCTGCTATGTATGGATTTAAATCGTAATCAT	3098
Db	3904	CCATGTGTTTCATCATCTTAAGTATTGTAAGCTGCTATGTATGGATTTAAACCGTAATCAT	3963
Qy	3099	ATTTGTTTTTCTGTATGAGGCACTGGTGAATAAACAAAGATCTGAGAAAGCTGTATATT	3158
Db	3964	A--TCTTTTTCCTATCTGAGGCACTGGTGGA-----ATAAAAAACCTGTATATT	4010
Qy	3159	ACACTTTGTGCGAGGTAGTCTTGCTGTAT-TTGGGGAATTGCAAAGAAAGTGGAGCTGAC	3217
Db	4011	TTACTTTGTTGCAGATAGTCTTGCCGCATCTTGCAAGTTGCAGAGATGGTGGAGCTAGA	4070
Qy	3218	AGAAATAA	3225
Db	4071	AAAAAAA	4078

AAZ56886

ID AAZ56886 standard; DNA; 3579 BP.

XX

AC AAZ56886;

XX

DT 25-APR-2000 (first entry)

XX

DE Human MAGI polypeptide encoding DNA.

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KW MAGI protein; neuroendocrine-specific protein; neuropathy; human;

KW spinal injury; neuronal degeneration; neuromuscular disorder; cancer;

KW psychiatric disorder; developmental disorder; inflammatory disorder;

KW stroke; cytostatic; cerebroprotective; neuroprotective; ds.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 1. .3579

FT /*tag= a

FT /product= "MAGI polypeptide"

XX

PN WO200005364-A1.

XX

PD 03-FEB-2000.

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PF 21-JUL-1999; 99WO-GB002360.

XX

PR 22-JUL-1998; 98GB-00016024.

PR 19-JUL-1999; 99GB-00016898.

XX

PA (SMIK) SMITHKLINE BEECHAM PLC.

XX

PI Michalovich D, Prinjha RK;

XX

DR WPI; 2000-182693/16.

DR P-PSDB; AAY56967.

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PT Novel polypeptides related to neuroendocrine-specific proteins and

PT polynucleotides useful for diagnosis of various diseases and for

PT treatment of cancer and neurological disorders.

XX

PS Claim 5; Page 19-20; 35pp; English.

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CC The invention relates to human MAGI protein, which is similar to
CC neuroendocrine-specific protein. The MAGI protein can be expressed by
CC standard recombinant methodology. The MAGI polypeptides, polynucleotides
CC and antibodies are useful for treating diseases, including neuropathies,
CC spinal injury, neuronal degeneration, neuromuscular disorders,
CC psychiatric disorders and developmental disorders, cancer, stroke and
CC inflammatory disorders. The polynucleotide is also useful for chromosome
CC localization and for tissue expression studies. The present sequence
CC represents a DNA encoding the human MAGI protein

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SQ Sequence 3579 BP; 1074 A; 803 C; 812 G; 890 T; 0 U; 0 Other;

Query Match 58.0%; Score 2223.6; DB 3; Length 3579;

Best Local Similarity 87.5%; Pred. No. 0;

Matches 2519; Conservative 0; Mismatches 339; Indels 22; Gaps 7;

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Qy      1 CTATCTCCTCTCTCAGCCGCTGCTTTTAAAGAACGTGAATACCTTGGTGATTTACCAGCA 60
      || |||||
Db     712 CTGTCTCCTCTCTCAGCCGCTTCTTTCAAAGAACATGAATACCTTGGTAATTTGTCAACA 771

Qy      61 GTACTGCCCACTGAAGGAACACTTCCAGCAACTTCAAATGAAGCTTCTAAAGCATTCTCA 120
      ||| | |||||
Db     772 GTATTACCCACTGAAGGAACACTTCAAGAAAATGTCAGTGAAGCTTCTAAAGAGGTCTCA 831

Qy     121 GAGAAGGCAAAAAATCCATTTGTAGAGAGAAATTTAACAGAATTTTCAGAATTGGAATAT 180
      |||||
Db     832 GAGAAGGCAAAAACTCTACTCATAGATAGAGATTTAACAGAGTTTTTCAGAATTAGAATAC 891

Qy     181 TCAGAAATGGAATCATCATTTCAGTGGCTCTCAAAAGGCAGAACCTGCCGTAACAGTAGCG 240
      |||||
Db     892 TCAGAAATGGGATCATCGTTTCAGTGTCTCTCCAAAAGCAGAATCTGCCGTAATAGTAGCA 951

Qy     241 AATCCTAGGGACGAAATAGTTGTGAGGAGTAGAGATAAAGAAGAGGACTTAGTTAGTCTT 300
      |||||
Db     952 AATCCTAGGGAAGAAATAATCGTGAAAAATAAAGATGAAGAAGAGAAGTTAGTTAGTAAT 1011

Qy     301 AACATCCTTCATACTCAGCAGGAGTTATCTACAGTCCTTACGAAATCAGTTGAAGAAGAA 360
      |||||
Db    1012 AACATCCTTCATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGGTTAAAGAGGAT 1071

Qy     361 GATAGAGTTCTGTCTCCAGAAAAACAAAGGACAGTTTTTAAGGAAAAGGGAGTTGCAGCA 420
      || |||||
Db    1072 GA---AGTTGTGTCTTCAGAAAAAGCAAAAGACAGTTTTTAATGAAAAGAGAGTTGCAGTG 1128

Qy     421 GAAGCTTCTATGGGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTG 480
      |||||
Db    1129 GAAGCTCCTATGAGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTG 1188

Qy     481 AAAGATACTTACAAGCAAGATAGTGATGTTTTGATTGCTGGAGGTAATATAGAGAGCAAA 540
      |||||
Db    1189 AAAGATAGT---AAGGAAGATAGTGATATGTTGGCTGCTGGAGGTAATAATCGAGAGCAAC 1245

Qy     541 TTGGAAGGTAAAGTGGATAAGAAACACTTTTCAGATAGCCTTGAACAAACAAATCGTGAA 600
      |||||
Db    1246 TTGGAAGGTAAAGTGGATAAAAAATGTTTTGCAGATAGCCTTGAACAACTAATCACGAA 1305

Qy     601 AAAGATAGTGAAAGCAGTAATGATGACACTTCATTTCCCAGTACACCAGAAGCTGTAAGA 660
      |||||
Db    1306 AAAGATAGTGAGAGTAGTAATGATGATACTTCTTTCCCCAGTACGCCAGAAGGTATAAAG 1365

Qy     661 GGTGGTTCCGGAGCGTACATCACGTGTGCTCCCTTTAACC---CAACAACAGAGAATGTT 717
      || |||||
Db    1366 GATCGTCCAGGAGCATATATCACATGTGCTCCCTTTAACCCAGCAGCAACTGAGAGCATT 1425

Qy     718 TCAACAAACATTTTCCCTTGTTGGAAGATCATACTTCGGAAAATAAGACAGATGAAAAA 777
      |||||
Db    1426 GCAACAAACATTTTCCCTTGTTAGGAGATCCTACTTCAGAAAATAAGACCGATGAAAAA 1485

Qy     778 AAGATAGAA-AAAAAAGGCACAAATTGTAACAGAGAAGAATGCAAGTGTAAGACATCA 836
      || |||||
Db    1486 AAAATAGAAGAAAAGAAGGCCCAATAGTAACAGAGAAGAATACTAGCACCAAAACATCA 1545
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Qy	837	AACCCCTTTTCCTTATGGCAGCACAGGAGTCTAAGACAGATTACGTTACAACAGATCATGTG	896
Db	1546	AACCCCTTTTCCTGTAGCAGCACAGGATTCTGAGACAGATTATGTCACAACAGATAATTTA	1605
Qy	897	TCAAAGGTGACCGAGGAAGTAGTGGCAAACATGCCTGAAGGTCTAACCCAGATTTGGTT	956
Db	1606	ACAAAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCCAGATTTAGTA	1665
Qy	957	CAGGAAGCATGTGAAAGTGAATTGAATGAAGCTACTGGTACAAAAATTGCCTTTGAAACA	1016
Db	1666	CAGGAAGCATGTGAAAGTGAATTGAATGAAGTTACTGGTACAAAGATTGCTTATGAAACA	1725
Qy	1017	AAAATGGACCTGGTTCAAACCTCAGAAGCTGTGCAGGAGTCACTTTACCCTGTAACACAG	1076
Db	1726	AAAATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCACAG	1785
Qy	1077	CTTTGCCCATCTTTTGAAGAATCTGAAGCTACTCCGTCACCGGTTTTGCCTGACATTGTC	1136
Db	1786	CTTTGCCCATCATTTGAAGAGTCAGAAGCTACTCCTTCACCAAGTTTTGCCTGACATTGTT	1845
Qy	1137	ATGGAAGCACCATTAAATTCTGTAGTTCCTAGTGCTGGTGCTTCTGCAGTGCAGCTCAGT	1196
Db	1846	ATGGAAGCACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGATACAGCCCAGC	1905
Qy	1197	TCATCACCATTAGAACTCTTCCTTCAGTTAATTATGAAAGCATAAAGTTTGAGCCTGAA	1256
Db	1906	TCATCACCATTAGAAGC---TTCTTCAGTTAATTATGAAAGCATAAAACATGAGCCTGAA	1962
Qy	1257	AATCCCCCACCATATGAGGAGGCCATGAATGTATCACTAAAAAAGAATCAGGAATGAAT	1316
Db	1963	AACCCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAGTATCAGGAATAAAG	2022
Qy	1317	GAAGAAATCACAGAGCCTGAAGGTATTAGTGTAGCTGTTCAGGAAACAGAAGCTCCTTAT	1376
Db	2023	GAAGAAATTAAAGAGCCTGAAAATATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTAT	2082
Qy	1377	ATATCTATTGCATGTGATTTAATTAAAGAAACAAAGATCTCTACTGAACCGACTCCAGAT	1436
Db	2083	ATATCTATTGCATGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAACCACTCCGGAT	2142
Qy	1437	TTCTCTAGTTATTCAGAAATAGCAGAAGTTGCACAGCCAGTGCCCCGAGCATTCTGAGCTA	1496
Db	2143	TTCTCTGATTATTCAGAAATGGCAAAAGTTGAACAGCCAGTGCCTGATCATTCTGAGCTA	2202
Qy	1497	GTTGAAGATTCCCTCCCCGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCC	1556
Db	2203	GTTGAAGATTCCCTCACCTGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCT	2262
Qy	1557	GAAGTTCCACAAAAACAAGATGAAGCTGTAATACTTGTGAAAGAAAACCTCACTGAAATT	1616
Db	2263	GACGTTCCACAAAAACAAGATGAAACTGTGATGCTTGTGAAAGAAAGTCTCACTGAGACT	2322
Qy	1617	TCATCTGAGTCAATGACAGGACATGACAATAAGGGAAAACTCAGTGCTTCACCATCACCT	1676
Db	2323	TCATTTGAGTCAATGATAGAATATGAAAATAAGGAAAACTCAGTGCTTTGC---CACCT	2379

Qy	1677	GAGGGAGGAAAACCGTATTTGGAGTCTTTTCAGCCCAGTTTAGGCATCACAAAAGATACC	1736
Db	2380	GAGGGAGGAAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATACC	2439
Qy	1737	TTAGCACCTGATGAAGTTTCAGCATTGACCCAAAAGGAGAAAATCCCTTTGCAGATGGAG	1796
Db	2440	CTGTTACCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAATTCCTTTGCAGATGGAG	2499
Qy	1797	GAGCTCAATACTGCAGTTTATTCAAGTGATGGCTTATTCATTGCTCAGGAAGCAAACCTA	1856
Db	2500	GAGCTCAGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGATA	2559
Qy	1857	AGAGAAAAGTGAAACATTTTCAGATTTCATCTCCGATTGAGATTATAGATGAGTTCCCGACC	1916
Db	2560	AGAGAAACTGAAACGTTTTCAGATTTCATCTCCAATTGAAATTATAGATGAGTTCCCTACA	2619
Qy	1917	TTTGTCTAGTTCTAAAGCAGATTCTTCTCCTACATTAGCCAGGGAATACACTGACCTAGAA	1976
Db	2620	TTGATCAGTTCTAAAAGTATTTCATTTTCTAAATTAGCCAGGGAATATACTGACCTAGAA	2679
Qy	1977	GTAGCCCAACAAAAGTGAAATTGCTGACATCCAGGATGGAGCTGGGTTCATTGGCTTGTGCA	2036
Db	2680	GTATCCCAACAAAAGTGAAATTGCTAATGCCCCGGATGGAGCTGGGTTCATTGCCTTGCACA	2739
Qy	2037	GGATTGCCCCATGACCTTTCTTTCAAGAGTATACAACC-----TAAAGAGGAAGTTCAT	2090
Db	2740	GAATTGCCCCATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCAGT	2799
Qy	2091	GTCCCAGATGAGTTCTCCAAAGATAGGGGTGATGTTTCAAAGGTGCCCGTACTGCCTCCA	2150
Db	2800	TTCTCAGATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCA	2859
Qy	2151	GATGTTTCTGCTTTGGATGCTCAAGCAGAGATAGGCAGCATAGAAAAACCCAAAGTTCTT	2210
Db	2860	GATGTTTCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTT	2919
Qy	2211	GTGAAAGAAGCCGAGAGAAAACTTCCTTCTGATACAGAAAAAGAGCGAAGATCTCCATCT	2270
Db	2920	GTGAAAGAAGCTGAGAAAAAACTTCCTTCCGATACAGAAAAAGAGGACAGATCACCATCT	2979
Qy	2271	GCTATATTTTCAGCAGAGCTGAGTAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGAC	2330
Db	2980	GCTATATTTTCAGCAGAGCTGAGTAAACTTCAGTTGTTGACCTCCTGTACTGGAGAGAC	3039
Qy	2331	ATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCTTGTTTCCTGCTGCTCTCGCTGACAGTA	2390
Db	3040	ATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCCTATTTCCTGCTGCTTTTATTGACAGTA	3099
Qy	2391	TTCAGCATTGTGAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCTGTGACTATCAGC	2450
Db	3100	TTCAGCATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGC	3159
Qy	2451	TTTAGGATATATAAGGGTGTGATCCAGGCTATCCAGAAATCTGATGAAGGCCACCCATTC	2510
Db	3160	TTTAGGATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTC	3219
Qy	2511	AGGGCATATTTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGCAAT	2570

Db	3220		AGGGCATATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGTAAT	3279
Qy	2571		TCTGCTCTTGGTCATGTAACTGCACAATAAAAGAACTCAGACGCCTCTTCTTAGTTGAT	2630
Db	3280		TCTGCTCTTGGTCATGTGAACTGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGAT	3339
Qy	2631		GATTTAGTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCC	2690
Db	3340		GATTTAGTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCC	3399
Qy	2691		TTGTTCAATGGTCTGACACTACTAATTTTGGCTCTGATTTCACTCTTCAGTGTTCCCTGTT	2750
Db	3400		TTGTTTAAATGGTCTGACACTACTGATTTTGGCTCTCATTTCACCTTCAGTGTTCCCTGTT	3459
Qy	2751		ATTTATGAACGGCATCAGGCGCAAATAGATCATTATCTGGGACTTGCAAATAAGAATGTT	2810
Db	3460		ATTTATGAACGGCATCAGGCGCAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTT	3519
Qy	2811		AAAGATGCTATGGCTAAAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGAATGA	2870
Db	3520		AAAGATGCTATGGCTAAAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGAATGA	3579

RESULT 9

AAF90324

ID AAF90324 standard; cDNA; 3579 BP.

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AC AAF90324;

XX

DT 23-JUL-2001 (first entry)

XX

DE Human NOGO-A cDNA.

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KW NOGO-A; human; chromosome 2p21; neuropathy; spinal injury; brain injury;
 KW stroke; neuronal degeneration; Alzheimer's disease; Parkinson's disease;
 KW neuromuscular disorder; psychiatric disorder; developmental disorder;
 KW neuroprotective; nootropic; neuroleptic; antiparkinsonian;
 KW cerebroprotective; neuroleptic; diagnosis; therapy; ss.

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OS Homo sapiens.

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PN WO200136631-A1.

XX

PD 25-MAY-2001.

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PF 14-NOV-2000; 2000WO-GB004345.

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PR 15-NOV-1999; 99GB-00026995.

PR 24-JAN-2000; 2000GB-00001550.

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PA (SMIK) SMITHKLINE BEECHAM PLC.

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PI Michalovich D, Prinjha R;

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DR WPI; 2001-343822/36.

DR P-PSDB; AAB82349.

Qy	1	CTATCTCCTCTCTCAGCCGCTGCTTTTAAAGAACGTGAATACCTTGGTGATTACCAGCA	60
Db	712	CTGTCTCCTCTCTCAGCCGCTTCTTTCAAAGAACATGAATACCTTGGTAATTTGTCAACA	771
Qy	61	GTACTGCCCACTGAAGGAACACTTCCAGCAACTTCAAATGAAGCTTCTAAAGCATTCTCA	120
Db	772	GTATTACCCACTGAAGGAACACTTCAAGAAAATGTCAAGTGAAGCTTCTAAAGAGGTCTCA	831
Qy	121	GAGAAGGCCAAAAATCCATTTGTAGAGAGAAATTTAACAGAATTTTCAGAATTGGAATAT	180
Db	832	GAGAAGGCCAAAACTCTACTCATAGATAGAGATTTAACAGAGTTTTTCAGAATTAGAATAC	891
Qy	181	TCAGAAATGGAATCATCATTTCAGTGGCTCTCAAAGGCAGAACCTGCCGTAACAGTAGCG	240
Db	892	TCAGAAATGGGATCATCGTTCAGTGTCTCTCCAAAGCAGAAATCTGCCGTAATAGTAGCA	951
Qy	241	AATCCTAGGGACGAAATAGTTGTGAGGAGTAGAGATAAGAAGAGGACTTAGTTAGTCTT	300
Db	952	AATCCTAGGGAAGAAATAATCGTGAAAAATAAAGATGAAGAAGAGAAGTTAGTTAGTAAT	1011
Qy	301	AACATCCTTCATACTCAGCAGGAGTTATCTACAGTCCTTACGAAATCAGTTGAAGAAGAA	360
Db	1012	AACATCCTTCATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGGTTAAAGAGGAT	1071
Qy	361	GATAGAGTTTCTGTCTCCAGAAAAACAAAGGACAGTTTTTAAGGAAAAGGGAGTTGCAGCA	420
Db	1072	GA---AGTTGTGTCTTCAGAAAAAGCAAAAGACAGTTTTTAATGAAAAGAGAGTTGCAGTG	1128

Qy	421	GAAGCTTCTATGGGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTG	480
Db	1129	GAAGCTCCTATGAGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTG	1188
Qy	481	AAAGATACTTACAAGCAAGATAGTGATGTTTTGATTGCTGGAGGTAATATAGAGAGCAAA	540
Db	1189	AAAGATAGT---AAGGAAGATAGTGATATGTTGGCTGCTGGAGGTAATATCGAGAGCAAC	1245
Qy	541	TTGGAAGGTAAAGTGGATAAGAAACACTTTTCAGATAGCCTTGAACAAACAAATCGTGAA	600
Db	1246	TTGGAAGGTAAAGTGGATAAAAAATGTTTTGCAGATAGCCTTGAACAACTAATCACGAA	1305
Qy	601	AAAGATAGTGAAAGCAGTAATGATGACACTTCATTTCCCAGTACACCAGAAGCTGTAAGA	660
Db	1306	AAAGATAGTGAGAGTAGTAATGATGATACTTCTTTCCCAGTACGCCAGAAGGTATAAAG	1365
Qy	661	GGTGGTTCGGAGCGTACATCACGTGTGCTCCCTTTAACC---CAACAACAGAGAATGTT	717
Db	1366	GATCGTCCAGGAGCATATATCACATGTGCTCCCTTTAACCAGCAGCAACTGAGAGCATT	1425
Qy	718	TCAACAAACATTTTTCCCTTGTTGGAAGATCATACTTCGAAAAATAAGACAGATGAAAAA	777
Db	1426	GCAACAAACATTTTTCCCTTGTTAGGAGATCCTACTTCAGAAAAATAAGACCGATGAAAAA	1485
Qy	778	AAGATAGAA-AAAAAAGGCACAAATTGTAACAGAGAAGAATGCAAGTGTCAAGACATCA	836
Db	1486	AAAATAGAAGAAAAGAAGGCCAAATAGTAACAGAGAAGAATACTAGCACCAAAACATCA	1545
Qy	837	AACCCTTTTCCTTATGGCAGCACAGGAGTCTAAGACAGATTACGTTACAACAGATCATGTG	896
Db	1546	AACCCTTTTCCTTGTAGCAGCACAGGATTCTGAGACAGATTATGTCACAACAGATAATTTA	1605
Qy	897	TCAAAGGTGACCGAGGAAGTAGTGGCAAACATGCCTGAAGGTCTAACCCCAGATTTGGTT	956
Db	1606	ACAAAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCCAGATTTAGTA	1665
Qy	957	CAGGAAGCATGTGAAAGTGAATTGAATGAAGCTACTGGTACAAAAATTGCCTTTGAAACA	1016
Db	1666	CAGGAAGCATGTGAAAGTGAATTGAATGAAGTTACTGGTACAAAGATTGCTTATGAAACA	1725
Qy	1017	AAAATGGACCTGGTTCAAACCTCAGAAGCTGTGCAGGAGTCACTTTACCCTGTAACACAG	1076
Db	1726	AAAATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCACAG	1785
Qy	1077	CTTTGCCCATCTTTTGAAGAATCTGAAGCTACTCCGTCACCGGTTTTGCCTGACATTGTC	1136
Db	1786	CTTTGCCCATCATTTGAAGAGTCAGAAGCTACTCCTTCACCAGTTTTGCCTGACATTGTT	1845
Qy	1137	ATGGAAGCACCATTAAATTCTGTAGTTCCTAGTGCTGGTGCTTCTGCAGTGCAGCTCAGT	1196
Db	1846	ATGGAAGCACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGATACAGCCCAGC	1905
Qy	1197	TCATCACCATTAGAAACTCTTCCTTCAGTTAATTATGAAAGCATAAAGTTTGAGCCTGAA	1256
Db	1906	TCATCACCATTAGAAGC---TTCTTCAGTTAATTATGAAAGCATAAAACATGAGCCTGAA	1962
Qy	1257	AATCCCCCACCATATGAGGAGGCCATGAATGTATCACTAAAAAAGAATCAGGAATGAAT	1316

Db	1963	AACCCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAGTATCAGGAATAAAG	2022
Qy	1317	GAAGAAATCACAGAGCCTGAAGGTATTAGTGTAGCTGTTCAAGAAACAGAAGCTCCTTAT	1376
Db	2023	GAAGAAATTAAAGAGCCTGAAAATATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTAT	2082
Qy	1377	ATATCTATTGCATGTGATTTAATTAAAGAAACAAAGATCTCTACTGAACCGACTCCAGAT	1436
Db	2083	ATATCTATTGCATGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAACCGACTCCGGAT	2142
Qy	1437	TTCTCTAGTTATTTCAGAAATAGCAGAAGTTGCACAGCCAGTGCCCGAGCATTCTGAGCTA	1496
Db	2143	TTCTCTGATTATTTCAGAAATGGCAAAAGTTGAACAGCCAGTGCCCTGATCATTCTGAGCTA	2202
Qy	1497	GTTGAAGATTCCCTCCCCGATTCTGAACCGATTGACTTATTTAGTGATGATTCAATACCC	1556
Db	2203	GTTGAAGATTCCCTCACCTGATTCTGAACCGATTGACTTATTTAGTGATGATTCAATACCT	2262
Qy	1557	GAAGTTCCACAAAAACAAGATGAAGCTGTAATACTTGTGAAAGAAAACCTCACTGAAATT	1616
Db	2263	GACGTTCCACAAAAACAAGATGAAACTGTGATGCTTGTGAAAGAAAGTCTCACTGAGACT	2322
Qy	1617	TCATCTGAGTCAATGACAGGACATGACAATAAGGGAAAACCTCAGTGCTTCACCATCACCT	1676
Db	2323	TCATTTGAGTCAATGATAGAATATGAAAATAAGGAAAACCTCAGTGCTTTGC---CACCT	2379
Qy	1677	GAGGGAGGAAAACCGTATTTGGAGTCTTTTCAGCCCAGTTTAGGCATCACAAAAGATACC	1736
Db	2380	GAGGGAGGAAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATACC	2439
Qy	1737	TTAGCACCTGATGAAGTTTCAGCATTGACCCAAAAGGAGAAAATCCCTTTGCAGATGGAG	1796
Db	2440	CTGTTACCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAATTCCTTTGCAGATGGAG	2499
Qy	1797	GAGCTCAATACTGCAGTTTATTCAAGTGATGGCTTATTCATTGCTCAGGAAGCAAACCTA	1856
Db	2500	GAGCTCAGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGATA	2559
Qy	1857	AGAGAAAAGTGAAACATTTTCAGATTTCATCTCCGATTGAGATTATAGATGAGTTCCCGACC	1916
Db	2560	AGAGAAAAGTGAAACGTTTTTCAGATTTCATCTCCAATTGAAATTATAGATGAGTTCCCTACA	2619
Qy	1917	TTTGTGAGTTCTAAAGCAGATTCTTCTCCTACATTAGCCAGGGAATACACTGACCTAGAA	1976
Db	2620	TTGATCAGTTCTAAAAGTATTCTTTCTAAATTAGCCAGGGAATATACTGACCTAGAA	2679
Qy	1977	GTAGCCCAAAAAGTGAAATTGCTGACATCCAGGATGGAGCTGGGTCATTGGCTTGTGCA	2036
Db	2680	GTATCCCAAAAAGTGAAATTGCTAATGCCCGGATGGAGCTGGGTCATTGCCTTGCACA	2739
Qy	2037	GGATTGCCCCATGACCTTTCTTTCAAGAGTATACAACC-----TAAAGAGGAAGTTCAT	2090
Db	2740	GAATTGCCCCATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCAGT	2799
Qy	2091	GTCCCGAGATGAGTTCTCCAAAGATAGGGGTGATGTTTCAAAGGTGCCCGTACTGCCTCCA	2150

Db	2800	TTCTCAGATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCA	2859
Qy	2151	GATGTTTCTGCTTTGGATGCTCAAGCAGAGATAGGCAGCATAGAAAAACCCAAAGTTCTT	2210
Db	2860	GATGTTTCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTT	2919
Qy	2211	GTGAAAGAAGCCGAGAGAAAACCTTCCTTCTGATACAGAAAAGAGCGAAGATCTCCATCT	2270
Db	2920	GTGAAAGAAGCTGAGAAAAAACTTCCTTCCGATACAGAAAAGAGGACAGATCACCATCT	2979
Qy	2271	GCTATATTTTCAGCAGAGCTGAGTAAAACCTTCAGTTGTTGACCTCCTCTACTGGAGAGAC	2330
Db	2980	GCTATATTTTCAGCAGAGCTGAGTAAAACCTTCAGTTGTTGACCTCCTGTACTGGAGAGAC	3039
Qy	2331	ATTAAGAAGACTGGAGTGGTGTGGTGCCAGCTTGTTCCCTGCTGCTCTCGCTGACAGTA	2390
Db	3040	ATTAAGAAGACTGGAGTGGTGTGGTGCCAGCCTATTCCTGCTGCTTTCATTGACAGTA	3099
Qy	2391	TTCAGCATTGTGAGTGTAACGGCCTACATTGCCTTGCCCTGCTCTCTGTGACTATCAGC	2450
Db	3100	TTCAGCATTGTGAGCGTAACAGCCTACATTGCCTTGCCCTGCTCTCTGTGACCATCAGC	3159
Qy	2451	TTTAGGATATATAAGGGTGTGATCCAGGCTATCCAGAAATCTGATGAAGGCCACCCATTC	2510
Db	3160	TTTAGGATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTC	3219
Qy	2511	AGGGCATATTTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGCAAT	2570
Db	3220	AGGGCATATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGTAAT	3279
Qy	2571	TCTGCTCTTGGTCATGTAACTGCACAATAAAAGAACTCAGACGCCTCTTCTTAGTTGAT	2630
Db	3280	TCTGCTCTTGGTCATGTGAACTGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGAT	3339
Qy	2631	GATTTAGTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCC	2690
Db	3340	GATTTAGTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCC	3399
Qy	2691	TTGTTCAATGGTCTGACACTACTAATTTTGGCTCTGATTTCACTCTTCAGTGTTCCCTGTT	2750
Db	3400	TTGTTAATGGTCTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTTCCCTGTT	3459
Qy	2751	ATTTATGAACGGCATCAGGCGCAAATAGATCATTATCTGGGACTTGCAAATAAGAATGTT	2810
Db	3460	ATTTATGAACGGCATCAGGCGCAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTT	3519
Qy	2811	AAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGAATGA	2870
Db	3520	AAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGAATGA	3579

RESULT 10

ABK90134

ID ABK90134 standard; DNA; 3579 BP.

XX

AC ABK90134;

XX

DT 21-OCT-2002 (first entry)
 XX
 DE DNA encoding human NogoA protein.
 XX
 KW Human; Nogo; BACE; acute neuronal injury; spinal injury; head injury;
 KW stroke; peripheral nerve damage; neoplastic disorder; glioblastoma;
 KW neuroblastoma; hyperproliferative disorder; dysproliferative disorder;
 KW cirrhosis; psoriasis; keloid formation; fibrocystic condition; cancer;
 KW tissue hypertrophy; central nervous system; axon regeneration; NogoA;
 KW Nogo-associated disease; metastasis; gene; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1. .3579
 FT /*tag= a
 FT /product= "Human NogoA protein"
 XX
 PN WO200257483-A2.
 XX
 PD 25-JUL-2002.
 XX
 PF 18-JAN-2002; 2002WO-GB000228.
 XX
 PR 18-JAN-2001; 2001GB-00001312.
 XX
 PA (GLAX) GLAXO GROUP LTD.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX
 PI Blackstock WP, Hale RS, Prinjha R, Rowley A;
 XX
 DR WPI; 2002-599722/64.
 DR P-PSDB; ABG30938.
 XX
 PT Identifying modulators of Nogo or BACE activity for treating acute
 PT neuronal injuries, neoplastic or dysproliferative disorders, comprises
 PT providing and monitoring interaction between Nogo and BACE polypeptides.
 XX
 PS Disclosure; Page 53-58; 68pp; English.
 XX
 CC The present invention relates to a new method of identifying modulators
 CC of Nogo function or BACE activity. The method involves providing Nogo and
 CC BACE polypeptides capable of binding with each other, monitoring the
 CC interaction between these polypeptides, and determining if the test agent
 CC is a modulator of Nogo or BACE activity. The method is useful in treating
 CC acute neuronal injuries, such as spinal or head injury, stroke,
 CC peripheral nerve damage, and in neoplastic (e.g. glioblastomas,
 CC neuroblastomas), hyperproliferative or dysproliferative disorders (e.g.
 CC cirrhosis, psoriasis, keloid formation, fibrocystic conditions, tissue
 CC hypertrophy) of the central nervous system. The BACE polypeptide is
 CC useful in screening methods to identify agents that may act as modulators
 CC of BACE activity and in particular agents that may be useful in treating
 CC Nogo-associated diseases. The modulators of Nogo or BACE polypeptides,
 CC and the polynucleotide encoding the BACE polypeptide are useful in
 CC manufacturing a medicament for the treatment or prevention of disorders
 CC responsive to the modulation of Nogo activity, in alleviating the
 CC symptoms or improving the condition of a patient suffering from this

CC disorder, in axon regeneration, or in preventing metastasis or spreading
CC of a cancer. The polynucleotide may also be an essential component in
CC assays, a probe, in recombinant protein synthesis, and in gene therapy
CC techniques. The present nucleic acid sequence encodes the human NogoA
CC protein of the invention

XX

SQ Sequence 3579 BP; 1074 A; 803 C; 812 G; 890 T; 0 U; 0 Other;

Query Match 58.0%; Score 2223.6; DB 6; Length 3579;
Best Local Similarity 87.5%; Pred. No. 0;
Matches 2519; Conservative 0; Mismatches 339; Indels 22; Gaps 7;

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Qy      1 CTATCTCCTCTCTCAGCCGCTGCTTTTAAAGAACGTGAATACCTTGGTGATTACCAAGCA 60
      || |||||
Db      712 CTGTCTCCTCTCTCAGCCGCTTCTTCAAAGAACATGAATACCTTGGTAATTTGTCAACA 771

Qy      61 GTACTGCCCCACTGAAGGAACACTTCCAGCAACTTCAAATGAAGCTTCTAAAGCATTCTCA 120
      ||| | |||||
Db      772 GTATTACCCACTGAAGGAACACTTCAAGAAAATGTCAGTGAAGCTTCTAAAGAGGTCTCA 831

Qy     121 GAGAAGGCAAAAAATCCATTTGTAGAGAGAAAATTTAACAGAATTTTCAGAATTGGAATAT 180
      |||||
Db     832 GAGAAGGCAAAAACTCTACTCATAGATAGAGATTTAACAGAGTTTTTCAGAATTAGAATAC 891

Qy     181 TCAGAAATGGAATCATCATTCAGTGGCTCTCAAAAGGCAGAACCTGCCGTAACAGTAGCG 240
      |||||
Db     892 TCAGAAATGGGATCATCGTTCAGTGTCTCTCCAAAAGCAGAAATCTGCCGTAATAGTAGCA 951

Qy     241 AATCCTAGGGACGAAATAGTTGTGAGGAGTAGAGATAAAGAAGAGGACTTAGTTAGTCTT 300
      |||||
Db     952 AATCCTAGGGAAGAAATAATCGTGAAAAATAAAGATGAAGAAGAGAAGTTAGTTAGTAAT 1011

Qy     301 AACATCCTTCATACTCAGCAGGAGTTATCTACAGTCCCTACGAAATCAGTTGAAGAAGAA 360
      |||||
Db    1012 AACATCCTTCATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGGTTAAAGAGGAT 1071

Qy     361 GATAGAGTTCTGTCTCCAGAAAAAACAAAGGACAGTTTTTAAGGAAAAGGGAGTTGCAGCA 420
      || |||||
Db    1072 GA---AGTTGTGTCTTCAGAAAAAGCAAAGACAGTTTTTAATGAAAAGAGAGTTGCAGTG 1128

Qy     421 GAAGCTTCTATGGGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTG 480
      |||||
Db    1129 GAAGCTCCTATGAGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTG 1188

Qy     481 AAAGATACTTACAAGCAAGATAGTGATGTTTTGATTGCTGGAGGTAATATAGAGAGCAAAA 540
      |||||
Db    1189 AAAGATAGT---AAGGAAGATAGTGATATGTTGGCTGCTGGAGGTAATAATCGAGAGCAAC 1245

Qy     541 TTGGAAGGTAAAGTGGATAAGAAACACTTTTCAGATAGCCTTGAACAAACAAATCGTGAA 600
      |||||
Db    1246 TTGGAAGTAAAGTGGATAAAAAATGTTTTGCAGATAGCCTTGAACAACTAATCACGAA 1305

Qy     601 AAAGATAGTGAAAGCAGTAATGATGACACTTCATTTCCCAGTACACCAGAAGCTGTAAGA 660
      |||||
Db    1306 AAAGATAGTGAGAGTAGTAATGATGATACTTCTTTCCCCAGTACGCCAGAAGGTATAAAG 1365

Qy     661 GGTGGTTCCGGAGCGTACATCACGTGTGCTCCCTTTAACC---CAACAACAGAGAATGTT 717
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Db	1366	GATCGTCCAGGAGCATATATCACATGTGCTCCCTTTAACCCAGCAGCAACTGAGAGCATT	1425
Qy	718	TCAACAAACATTTTTCCCTTGTTGGAAGATCATACTTCGGAAAATAAGACAGATGAAAAA	777
Db	1426	GCAACAAACATTTTTCTTTGTTAGGAGATCCTACTTCAGAAAATAAGACCGATGAAAAA	1485
Qy	778	AAGATAGAA-AAAAAAAGGCACAAATTGTAACAGAGAAGAATGCAAGTGTCAGACATCA	836
Db	1486	AAAATAGAAGAAAAGAAGGCCCAAATAGTAACAGAGAAGAATACTAGCACAAAACATCA	1545
Qy	837	AACCCCTTTCCTTATGGCAGCACAGGAGTCTAAGACAGATTACGTTACAACAGATCATGTG	896
Db	1546	AACCCCTTTTCTTGTAGCAGCACAGGATTCTGAGACAGATTATGTGCACAACAGATAATTTA	1605
Qy	897	TCAAAGGTGACCGAGGAAGTAGTGGCAAACATGCCTGAAGGTCTAACCCAGATTTGGTT	956
Db	1606	ACAAAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCCAGATTTAGTA	1665
Qy	957	CAGGAAGCATGTGAAAGTGAATTGAATGAAGCTACTGGTACAAAAATTGCCTTTGAAACA	1016
Db	1666	CAGGAAGCATGTGAAAGTGAATTGAATGAAGTTACTGGTACAAAGATTGCTTATGAAACA	1725
Qy	1017	AAAATGGACCTGGTTCAAACCTCAGAAGCTGTGCAGGAGTCACTTTACCCTGTAACACAG	1076
Db	1726	AAAATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCACAG	1785
Qy	1077	CTTTGCCCATCTTTTGAAGAATCTGAAGCTACTCCGTCACCGGTTTTGCCTGACATTGTC	1136
Db	1786	CTTTGCCCATCATTTGAAGAGTCAGAAGCTACTCCTTCACCAGTTTTGCCTGACATTGTT	1845
Qy	1137	ATGGAAGCACCATTAAATTCTGTAGTTCCTAGTGCTGGTGCTTCTGCAGTGCAGCTCAGT	1196
Db	1846	ATGGAAGCACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGATACAGCCCAGC	1905
Qy	1197	TCATCACCATTAGAACTCTTCCTTCAGTTAATTATGAAAGCATAAAAGTTTGAGCCTGAA	1256
Db	1906	TCATCACCATTAGAAGC---TTCTTCAGTTAATTATGAAAGCATAAAACATGAGCCTGAA	1962
Qy	1257	AATCCCCCACCATATGAGGAGGCCATGAATGTATCACTAAAAAAGAATCAGGAATGAAT	1316
Db	1963	AACCCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAGTATCAGGAATAAAG	2022
Qy	1317	GAAGAAATCACAGAGCCTGAAGGTATTAGTGTAGCTGTTTCAGGAAACAGAAGCTCCTTAT	1376
Db	2023	GAAGAAATTAAAGAGCCTGAAAATATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTAT	2082
Qy	1377	ATATCTATTGCATGTGATTTAATTAAAGAAACAAAGATCTCTACTGAACCGACTCCAGAT	1436
Db	2083	ATATCTATTGCATGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAACCAGCTCCGGAT	2142
Qy	1437	TTCTCTAGTTATTTCAGAAATAGCAGAAGTTGCACAGCCAGTGCCCGAGCATTCTGAGCTA	1496
Db	2143	TTCTCTGATTATTTCAGAAATGGCAAAAGTTGAACAGCCAGTGCCTGATCATTCTGAGCTA	2202
Qy	1497	GTTGAAGATTCCCTCCCCGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCC	1556

Db	2203	GTGAAGATTCCCTCACCTGATTCTGAACCAAGTTGACTTATTTAGTGATGATTCAATACCT	2262
Qy	1557	GAAGTTCCACAAAAACAAGATGAAGCTGTAATACTTGTGAAAGAAAACCTCACTGAAATT	1616
Db	2263	GACGTTCCACAAAAACAAGATGAACTGTGATGCTTGTGAAAGAAAGTCTCACTGAGACT	2322
Qy	1617	TCATCTGAGTCAATGACAGGACATGACAATAAGGGAAAACCTCAGTGCTTCACCATCACCT	1676
Db	2323	TCATTTGAGTCAATGATAGAATATGAAAATAAGGAAAAAAGTCTCAGTGCTTTGCG---CACCT	2379
Qy	1677	GAGGGAGGAAAACCGTATTTGGAGTCTTTTCAGCCCAGTTTAGGCATCACAAAAGATAACC	1736
Db	2380	GAGGGAGGAAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATAACC	2439
Qy	1737	TTAGCACCTGATGAAGTTTCAGCATTGACCCAAAAGGAGAAAATCCCTTTGCAGATGGAG	1796
Db	2440	CTGTTACCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAATTCCTTTGCAGATGGAG	2499
Qy	1797	GAGCTCAATACTGCAGTTTATTCAAGTGATGGCTTATTGCTCAGGAAGCAAACCTA	1856
Db	2500	GAGCTCAGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGATA	2559
Qy	1857	AGAGAAAGTGAAACATTTTCAGATTCATCTCCGATTGAGATTATAGATGAGTTCCCGACC	1916
Db	2560	AGAGAAACTGAAACGTTTTTCAGATTCATCTCCAATTGAAATTATAGATGAGTTCCCTACA	2619
Qy	1917	TTTGTGAGTTCTAAAGCAGATTCTTCTCCTACATTAGCCAGGGAATACACTGACCTAGAA	1976
Db	2620	TTGATCAGTTCTAAACTGATTCATTTTCTAAATTAGCCAGGGAATATACTGACCTAGAA	2679
Qy	1977	GTAGCCACAAAAGTGAAATTGCTGACATCCAGGATGGAGCTGGGTGCTTGGCTTGTGCA	2036
Db	2680	GATCCACAAAAGTGAAATTGCTAATGCCCCGGATGGAGCTGGGTGCTTGCCTTGACACA	2739
Qy	2037	GGATTGCCCCATGACCTTTCTTTCAAGAGTATACAACC-----TAAAGAGGAAGTTCAT	2090
Db	2740	GAATTGCCCCATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCAGT	2799
Qy	2091	GTCCCAGATGAGTTCTCCAAAGATAGGGGTGATGTTTCAAAGGTGCCCCGACTGCCTCCA	2150
Db	2800	TTCTCAGATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCA	2859
Qy	2151	GATGTTTCTGCTTTGGATGCTCAAGCAGAGATAGGCAGCATAGAAAAACCCAAAGTTCTT	2210
Db	2860	GATGTTTCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTT	2919
Qy	2211	GTGAAAGAAGCCGAGAGAAAACCTCCTTCTGATACAGAAAAAGAGCGAAGATCTCCATCT	2270
Db	2920	GTGAAAGAAGCTGAGAAAAACCTCCTTCCGATACAGAAAAAGAGGACAGATCACCATCT	2979
Qy	2271	GCTATATTTTCAGCAGAGCTGAGTAAACCTTCAGTTGTTGACCTCCTCTACTGGAGAGAC	2330
Db	2980	GCTATATTTTCAGCAGAGCTGAGTAAACCTTCAGTTGTTGACCTCCTGTACTGGAGAGAC	3039
Qy	2331	ATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCTTGTTTCTGCTGCTCTCGCTGACAGTA	2390
Db	3040	ATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCCTATTCTGCTGCTTTTCATTGACAGTA	3099

Qy	2391	TTCAGCATTGTGAGTGTAAACGGCCTACATTGCCTTGGCCCTGCTCTCTGTGACTATCAGC	2450
Db	3100	TTCAGCATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGC	3159
Qy	2451	TTTAGGATATATAAGGGTGTGATCCAGGCTATCCAGAAATCTGATGAAGGCCACCCATTC	2510
Db	3160	TTTAGGATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTC	3219
Qy	2511	AGGGCATATTTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGCAAT	2570
Db	3220	AGGGCATATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGTAAT	3279
Qy	2571	TCTGCTCTTGGTCATGTTAACTGCACAATAAAAGAACTCAGACGCCTCTTCTTAGTTGAT	2630
Db	3280	TCTGCTCTTGGTCATGTGAAGTGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGAT	3339
Qy	2631	GATTTAGTTGATTCTCTGAAGTTTGCAGTGTGATGTGGGTATTTACCTATGTTGGTGCC	2690
Db	3340	GATTTAGTTGATTCTCTGAAGTTTGCAGTGTGATGTGGGTATTTACCTATGTTGGTGCC	3399
Qy	2691	TTGTTCAATGGTCTGACACTACTAATTTTGGCTCTGATTTCACTCTTCAGTGTTCCTGTT	2750
Db	3400	TTGTTAATGGTCTGACACTACTGATTTTGGCTCTCATTTCCTTCAGTGTTCCTGTT	3459
Qy	2751	ATTTATGAACGGCATCAGGCGCAAATAGATCATTATCTGGGACTTGCAAATAAGAATGTT	2810
Db	3460	ATTTATGAACGGCATCAGGCGCAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTT	3519
Qy	2811	AAAGATGCTATGGCTAAATCCAAGCAAAATCCCTGGATTGAAGCGTAAAGCTGAATGA	2870
Db	3520	AAAGATGCTATGGCTAAATCCAAGCAAAATCCCTGGATTGAAGCGTAAAGCTGAATGA	3579

RESULT 11

ABN86601

ID ABN86601 standard; DNA; 3579 BP.

XX

AC ABN86601;

XX

DT 05-NOV-2002 (first entry)

XX

DE Human neurotransmitter receptor protein Nogo encoding DNA.

XX

KW Nerve regeneration; neuroprotection; neuronal degeneration; CNS; PNS;
 KW central nervous system; peripheral nervous system; tranquillizer; Nogo;
 KW vulnerary; cerebroprotective; anti-tumour; antidiabetic; anticonvulsant;
 KW nootropic; antiparkinsonian; ophthalmological; analgesic; hepatotropic;
 KW osteopathic; vasotropic; nephrotropic; cytostatic; antigen; gene therapy;
 KW neurotransmitter receptor; human; gene; ds.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 1..3579

FT /*tag= a

FT /product= "Nogo"

FT /note= "Nogo-A, Nogo-B and Nogo-C"
 XX
 PN US2002072493-A1.
 XX
 PD 13-JUN-2002.
 XX
 PF 28-JUN-2001; 2001US-00893348.
 XX
 PR 19-MAY-1998; 98IL-00124500.
 PR 21-JUL-1998; 98WO-US014715.
 PR 22-DEC-1998; 98US-00218277.
 PR 19-MAY-1999; 99US-00314161.
 XX
 PA (YEDA) YEDA RES & DEV CO LTD.
 XX
 PI Eisenbach-Schwartz M, Hauben E, Cohen IR, Beserman P, Mosonego A;
 PI Moalem G;
 XX
 DR WPI; 2002-607255/65.
 DR P-PSDB; ABB81078, ABB81079, ABB81080.
 XX
 PT Promoting nerve regeneration and preventing neuronal degeneration in the
 PT central/peripheral nervous system from injury/disease, comprises
 PT administering nervous system-specific activated T cells/antigen, or
 PT analogs/peptides.
 XX
 PS Disclosure; Page 49-53; 93pp; English.
 XX
 CC The invention relates to promoting nerve regeneration or conferring
 CC neuroprotection and preventing or inhibiting neuronal degeneration in the
 CC central/peripheral nervous system (NS). The method involves administering
 CC NS-specific activated T cells, NS-specific antigen, its analogue or its
 CC peptide, a nucleotide sequence the NS-specific antigen or its analogue or
 CC combinations. The method is useful for promoting nerve regeneration and
 CC preventing neuronal degeneration in central/peripheral nervous system
 CC from injury/disease, where the injury is spinal cord injury, blunt
 CC trauma, penetrating trauma, hemorrhagic stroke, ischaemic stroke or
 CC damages caused by surgery such as tumour excision. The disease is not an
 CC autoimmune disease or neoplasm. The disease results in a degenerative
 CC process occurring in either gray or white matter or both. The disease is
 CC diabetic neuropathy, senile dementia, Alzheimer's disease, Parkinson's
 CC disease, facial nerve (Bell's) palsy, glaucoma, Huntington's chorea,
 CC amyotrophic lateral sclerosis, non-arteritic optic neuropathy, and
 CC vitamin deficiency, intervertebral disc herniation, prion diseases such
 CC as Creutzfeldt-Jakob disease, carpal tunnel syndrome, peripheral
 CC neuropathies associated with various diseases, including but not limited
 CC to uremia, porphyria, hypoglycemia, Sjorgren Larsson syndrome, acute
 CC sensory neuropathy, chronic ataxic neuropathy, biliary cirrhosis, primary
 CC amyloidosis, obstructive lung diseases, acromegaly, malabsorption
 CC syndromes, polycythemia vera, immunoglobulin (Ig)A- and IgG gamma-
 CC pathies, complications of various drugs (e.g., metronidazole) and toxins
 CC (e.g., alcohol or organophosphates), Charcot-Marie-Tooth disease, ataxia
 CC telangiectasia, Friedreich's ataxia, amyloid polyneuropathies,
 CC adrenomyeloneuropathy, Giant axonal neuropathy, Refsum's disease, Fabry's
 CC disease, or lipoproteinemia. The present sequence represents a DNA
 CC encoding the human neurotransmitter receptor protein Nogo (Nogo-A, Nogo-B
 CC and Nogo-C), an example of NS-specific antigen

XX

SQ Sequence 3579 BP; 1074 A; 803 C; 812 G; 890 T; 0 U; 0 Other;

Query Match 58.0%; Score 2223.6; DB 6; Length 3579;
Best Local Similarity 87.5%; Pred. No. 0;
Matches 2519; Conservative 0; Mismatches 339; Indels 22; Gaps 7;

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Qy      1 CTATCTCCTCTCTCAGCCGCTGCTTTTAAAGAACGTGAATACCTTGGTGATTTACCAGCA 60
      || |||||
Db      712 CTGTCTCCTCTCTCAGCCGCTTCTTTCAAAGAACATGAATACCTTGGTAATTTGTCAACA 771

Qy      61 GTACTGCCCCACTGAAGGAACACTTCCAGCAACTTCAAATGAAGCTTCTAAAGCATTCTCA 120
      ||| | |||||
Db      772 GTATTACCCACTGAAGGAACACTTCAAGAAAATGTCAGTGAAGCTTCTAAAGAGGTCTCA 831

Qy     121 GAGAAGGCCAAAAATCCATTTGTAGAGAGAAATTTAACAGAATTTTCAGAATTGGAATAT 180
      |||||
Db     832 GAGAAGGCCAAAACTCTACTCATAGATAGAGATTTAACAGAGTTTTCAGAATTAGAATAC 891

Qy     181 TCAGAAATGGAATCATCATTCAGTGGCTCTCAAAAGGCAGAACCTGCCGTAACAGTAGCG 240
      |||||
Db     892 TCAGAAATGGGATCATCGTTTCAGTGTCTCTCCAAAAGCAGAACTCTGCCGTAATAGTAGCA 951

Qy     241 AATCCTAGGGACGAAATAGTTGTGAGGAGTAGAGATAAAGAAGAGGACTTAGTTAGTCTT 300
      |||||
Db     952 AATCCTAGGGAAGAAATAATCGTGAAAAATAAAGATGAAGAAGAGAAGTTAGTTAGTAAT 1011

Qy     301 AACATCCTTCATACTCAGCAGGAGTTATCTACAGTCCTTACGAAATCAGTTGAAGAAGAA 360
      |||||
Db    1012 AACATCCTTCATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGGTTAAAGAGGAT 1071

Qy     361 GATAGAGTTCTGTCTCCAGAAAAACAAAGGACAGTTTTAAGGAAAAGGGAGTTGCAGCA 420
      || |||||
Db    1072 GA---AGTTGTGTCTTCAGAAAAAGCAAAGACAGTTTTAATGAAAAGAGAGTTGCAGTG 1128

Qy     421 GAAGCTTCTATGGGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTG 480
      |||||
Db    1129 GAAGCTCCTATGAGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTG 1188

Qy     481 AAAGATACTTACAAGCAAGATAGTGATGTTTTGATTGCTGGAGGTAATATAGAGAGCAAA 540
      |||||
Db    1189 AAAGATAGT---AAGGAAGATAGTGATATGTTGGCTGCTGGAGGTAATATCGAGAGCAAC 1245

Qy     541 TTGGAAGGTAAAGTGGATAAGAAACACTTTTCAGATAGCCTTGAACAAACAAATCGTGAA 600
      |||||
Db    1246 TTGGAAGGTAAAGTGGATAAAAAATGTTTTGCAGATAGCCTTGAACAACTAATCACGAA 1305

Qy     601 AAAGATAGTGAAAGCAGTAATGATGACACTTCATTTCCAGTACACCAGAAGCTGTAAGA 660
      |||||
Db    1306 AAAGATAGTGAGAGTAGTAATGATGATACTTCTTTCCCGAGTACGCCAGAAGGTATAAAG 1365

Qy     661 GGTGGTTCCGGAGCGTACATCACGTGTGCTCCCTTTAACC---CAACAAGTGAAGTGT 717
      || |||
Db    1366 GATCGTCCAGGAGCATATATCACATGTGCTCCCTTTAACCCAGCAGCAACTGAGAGCATT 1425

Qy     718 TCAACAAACATTTTCCCTTGTTGGAAGATCATACTTCGGAAAATAAGACAGATGAAAAA 777
      |||||
```

Db	1426	GCAACAAACATTTTTTCCTTTGTTAGGAGATCCTACTTCAGAAAAATAAGACCGATGAAAAA	1485
Qy	778	AAGATAGAA-AAAAAAGGCACAAATTGTAACAGAGAAGAATGCAAGTGTCAAGACATCA	836
Db	1486	AAAATAGAAGAAAAGAAGGCCCAAATAGTAACAGAGAAGAATACTAGCACCAAACATCA	1545
Qy	837	AACCCCTTTCCTTATGGCAGCACAGGAGTCTAAGACAGATTACGTTACAACAGATCATGTG	896
Db	1546	AACCCCTTTCCTTGTAGCAGCACAGGATTCTGAGACAGATTATGTCACAACAGATAATTTA	1605
Qy	897	TCAAAGGTGACCGAGGAAGTAGTGGCAAACATGCCTGAAGGTCTAACCCAGATTTGGTT	956
Db	1606	ACAAAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCCAGATTTAGTA	1665
Qy	957	CAGGAAGCATGTGAAAAGTGAATTGAATGAAGCTACTGGTACAAAAATTGCCTTTGAAACA	1016
Db	1666	CAGGAAGCATGTGAAAAGTGAATTGAATGAAGTTACTGGTACAAAGATTGCTTATGAAACA	1725
Qy	1017	AAAATGGACCTGGTTCAAACTTCAGAAGCTGTGCAGGAGTCACTTTACCCTGTAACACAG	1076
Db	1726	AAAATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCACAG	1785
Qy	1077	CTTTGCCCATCTTTTGAAGAATCTGAAGCTACTCCGTCAACGGTTTTGCCTGACATTGTC	1136
Db	1786	CTTTGCCCATCATTTGAAGAGTCAGAAGCTACTCCTTCACCAGTTTTGCCTGACATTGTT	1845
Qy	1137	ATGGAAGCACCATTAAATTCTGTAGTTCCTAGTGCTGGTGCTTCTGCAGTGCAGCTCAGT	1196
Db	1846	ATGGAAGCACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGATACAGCCCAGC	1905
Qy	1197	TCATCACCATTAGAAACTCTTCCTTCAGTTAATTATGAAAGCATAAAGTTTGAGCCTGAA	1256
Db	1906	TCATCACCATTAGAAGC---TTCTTCAGTTAATTATGAAAGCATAAAACATGAGCCTGAA	1962
Qy	1257	AATCCCCCACCATATGAGGAGGCCATGAATGTATCACTAAAAAAGAATCAGGAATGAAT	1316
Db	1963	AACCCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAGTATCAGGAATAAAG	2022
Qy	1317	GAAGAAATCACAGAGCCTGAAGGTATTAGTGTAGCTGTTTCAGGAAACAGAAGCTCCTTAT	1376
Db	2023	GAAGAAATTAAAGAGCCTGAAAATATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTAT	2082
Qy	1377	ATATCTATTGCATGTGATTTAATTAAAGAAACAAAGATCTCTACTGAACCGACTCCAGAT	1436
Db	2083	ATATCTATTGCATGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAACCGACTCCGGAT	2142
Qy	1437	TTCTCTAGTTATTCAGAAATAGCAGAAGTTGCACAGCCAGTGCCCGAGCATTCTGAGCTA	1496
Db	2143	TTCTCTGATTATTCAGAAATGGCAAAGTTGAACAGCCAGTGCCCTGATCATTTCTGAGCTA	2202
Qy	1497	GTTGAAGATTCCCTCCCCGATTCTGAACCAGTTGACTTATTTAGTGTGATGATTCAATACCC	1556
Db	2203	GTTGAAGATTCCCTCACCTGATTCTGAACCAGTTGACTTATTTAGTGTGATGATTCAATACCT	2262
Qy	1557	GAAGTTCACAAAAACAAGATGAAGCTGTAATACTTGTGAAAGAAAACCTCACTGAAATT	1616
Db	2263	GACGTTTCACAAAAACAAGATGAAACTGTGATGCTTGTGAAAGAAAGTCTCACTGAGACT	2322

Qy	1617	TCATCTGAGTCAATGACAGGACATGACAATAAGGGGAAAACCTCAGTGCTTCACCATCACCT	1676
Db	2323	TCATTTGAGTCAATGATAGAATATGAAAATAAGGAAAAACCTCAGTGCTTTGC---CACCT	2379
Qy	1677	GAGGGAGGAAAACCGTATTTGGAGTCTTTTCAGCCCAGTTTAGGCATCACAAAAGATACC	1736
Db	2380	GAGGGAGGAAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATACC	2439
Qy	1737	TTAGCACCTGATGAAGTTTCAGCATTGACCCAAAAGGAGAAAATCCCTTTGCAGATGGAG	1796
Db	2440	CTGTTACCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAATTCCTTTGCAGATGGAG	2499
Qy	1797	GAGCTCAATACTGCAGTTTATTCAAGTGATGGCTTATTTCATTGCTCAGGAAGCAAACCTA	1856
Db	2500	GAGCTCAGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGATA	2559
Qy	1857	AGAGAAAAGTGAAACATTTTCAGATTTCATCTCCGATTGAGATTATAGATGAGTTCCCGACC	1916
Db	2560	AGAGAAAACCTGAAACGTTTTCAGATTTCATCTCCAATTGAAATTATAGATGAGTTCCCTACA	2619
Qy	1917	TTTGTCAGTTCTAAAAGCAGATTCTTCTCCTACATTAGCCAGGGAATACACTGACCTAGAA	1976
Db	2620	TTGATCAGTTCTAAAACCTGATTTCATTTCTAAATTAGCCAGGGAATATACTGACCTAGAA	2679
Qy	1977	GTAGCCACAAAAGTGAAATTGCTGACATCCAGGATGGAGCTGGGTTCATTGGCTTGTGCA	2036
Db	2680	GTATCCACAAAAGTGAAATTGCTAATGCCCCGGATGGAGCTGGGTTCATTGCCTTGCACA	2739
Qy	2037	GGATTGCCCCATGACCTTTCTTTCAAGAGTATACAACC-----TAAAGAGGAAGTTCAT	2090
Db	2740	GAATTGCCCCATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCAGT	2799
Qy	2091	GTCCCAGATGAGTTCTCCAAAGATAGGGGTGATGTTTCAAAGGTGCCCCGTA CTGCCTCCA	2150
Db	2800	TTCTCAGATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCA	2859
Qy	2151	GATGTTTCTGCTTTGGATGCTCAAGCAGAGATAGGCAGCATAGAAAAACCCAAAGTTCTT	2210
Db	2860	GATGTTTCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTT	2919
Qy	2211	GTGAAAGAAGCCGAGAGAAAACCTTCCTTCTGATACAGAAAAAGAGCGAAGATCTCCATCT	2270
Db	2920	GTGAAAGAAGCTGAGAAAAAACCTTCCTTCCGATACAGAAAAAGAGGACAGATCACCATCT	2979
Qy	2271	GCTATATTTTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGAC	2330
Db	2980	GCTATATTTTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTGTACTGGAGAGAC	3039
Qy	2331	ATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCTTGTTTCCTGCTGCTCTCGCTGACAGTA	2390
Db	3040	ATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCCTATTCTGCTGCTTTTCATTGACAGTA	3099
Qy	2391	TTCAGCATTGTGAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCTGTGACTATCAGC	2450
Db	3100	TTCAGCATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGC	3159

Qy	2451	TTTAGGATATATAAGGGTGTGATCCAGGCTATCCAGAAATCTGATGAAGGCCACCCATTC	2510
Db	3160	TTTAGGATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTC	3219
Qy	2511	AGGGCATATTTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGCAAT	2570
Db	3220	AGGGCATATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGTAAT	3279
Qy	2571	TCTGCTCTTGGTCATGTTAAGTGCACAATAAAAGAACTCAGACGCCTCTTCTTAGTTGAT	2630
Db	3280	TCTGCTCTTGGTCATGTGAAGTGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGAT	3339
Qy	2631	GATTTAGTTGATTCTCTGAAGTTTGCAGTGTGATGTGGGTATTTACCTATGTTGGTGCC	2690
Db	3340	GATTTAGTTGATTCTCTGAAGTTTGCAGTGTGATGTGGGTATTTACCTATGTTGGTGCC	3399
Qy	2691	TTGTTCAATGGTCTGACACTACTAATTTTGGCTCTGATTTCACTCTTCAGTGTTCCTGTT	2750
Db	3400	TTGTTTAATGGTCTGACACTACTGATTTTGGCTCTCATTTCCTTCAGTGTTCCTGTT	3459
Qy	2751	ATTTATGAACGGCATCAGGCGCAAATAGATCATTATCTGGGACTTGCAAATAAGAATGTT	2810
Db	3460	ATTTATGAACGGCATCAGGCGCAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTT	3519
Qy	2811	AAAGATGCTATGGCTAAAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGAATGA	2870
Db	3520	AAAGATGCTATGGCTAAAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGAATGA	3579

RESULT 12

AAD01173

ID AAD01173 standard; cDNA; 4684 BP.

XX

AC AAD01173;

XX

DT 02-NOV-2000 (first entry)

XX

DE Rat neurite growth inhibitor Nogo A cDNA.

XX

KW Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;
 KW central nervous system; neoplastic disease; antiproliferative; glioma;
 KW antisense gene therapy; neuroblastoma; menagioma; retinoblastoma;
 KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;
 KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;
 KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
 KW structural plasticity; screening; ss.

XX

OS Rattus sp.

XX

FH Key Location/Qualifiers

FT CDS 253. .3744

FT /*tag= a

FT /product= "Nogo A"

FT /transl_except= (pos:1462. .1464, aa:Ile)

XX

PN WO200031235-A2.

XX

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PD 02-JUN-2000.
XX
PF 05-NOV-1999; 99WO-US026160.
XX
PR 06-NOV-1998; 98US-0107446P.
XX
PA (SCHW/) SCHWAB M E.
PA (CHEN/) CHEN M S.
XX
PI Schwab ME, Chen MS;
XX
DR WPI; 2000-400052/34.
DR P-PSDB; AAY71310.
XX
PT Nogo proteins and nucleic acids useful for treating neoplastic disorders
PT of the central nervous system and inducing regeneration of neurons.
XX
PS Claim 26; Fig 2A; 122pp; English.
XX
CC The present sequence is a cDNA encoding rat Nogo A protein which is a
CC potent neural cell growth inhibitor and is free of all central nervous
CC system (CNS) myelin material with which it is natively associated. The
CC present sequence was generated by fusing R018U37-3, R1-3U21 cDNA
CC sequences isolated from hexanucleotides-primed rat brain stem/spinal cord
CC library, and Ol18 cDNA from an oligo d(T)-primed rat oligodendrocyte
CC library. Nogo proteins and fragments displaying neurite growth inhibitory
CC activity are used in the treatment of neoplastic disease of the CNS e.g.
CC glioma, glioblastoma, medulloblastoma, craniopharyngioma, ependyoma,
CC pinealoma, haemangioblastoma, acoustic neuroma, oligodendroglioma,
CC menagioma, neuroblastoma or retinoblastoma and degenerative nerve
CC diseases e.g. Alzheimer's and Parkinson's diseases. Therapeutics which
CC promote Nogo activity can be used to treat or prevent hyperproliferative
CC or benign dysproliferative disorders e.g. psoriasis and tissue
CC hypertrophy. Ribozymes or antisense Nogo nucleic acids can be used to
CC inhibit production of Nogo protein to induce regeneration of neurons or
CC to promote structural plasticity of the CNS in disorders where neurite
CC growth, regeneration or maintenance are deficient or desired. The animal
CC models can be used in diagnostic and screening methods for predisposition
CC to disorders and to screen for or test molecules which can treat or
CC prevent disorders or diseases of the CNS. Note: SEQ ID numbers 35-42 are
CC referred in claim 32 and SEQ ID NO: 29 in disclosure of the
CC specification. However the specification does not include sequences for
CC these SEQ ID numbers
XX
SQ Sequence 4684 BP; 1358 A; 1048 C; 1112 G; 1166 T; 0 U; 0 Other;

Query Match 57.0%; Score 2183.4; DB 3; Length 4684;
Best Local Similarity 78.0%; Pred. No. 0;
Matches 3004; Conservative 0; Mismatches 736; Indels 109; Gaps 27;

Qy 1 CTATCTCCTCTCTCAGCCGCTGCTTTTAAAGAACGTGAATACCTTGGTGATTTACCAGCA 60
Db 928 CTATCTCCTCTCTCAACTGTTTCTTTTAAAGAACATGGATACCTTGGTAACTTATCAGCA 987

Qy 61 GTACTGCCCCACTGAAGGAACACTTCCAGCAAACTTCAAATGAAGCTTCTAAAGCATTTCTCA 120
Db 988 GTGTCATCCTCAGAAGGAACAATTGAAGAACTTTAAATGAAGCTTCTAAAGAGTTGCCA 1047

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Qy	121	GAGAAGGCCAAAAATCCATTTGTAGAGAGAAATTTAACAGAATTTTCAGAATTGGAATAT	180
Db	1048	GAGAGGGCAACAAATCCATTTGTAAATAGAGATTTAGCAGAATTTTCAGAATTAGAATAT	1107
Qy	181	TCAGAAATGGAATCATCATTCACTGGCTCTCAAAGGCAGAACCTGCCGTAACAGTAGCG	240
Db	1108	TCAGAAATGGGATCATCTTTTAAAGGCTCCCCAAAAGGAGAGTCAGCCATATTAGTAGAA	1167
Qy	241	AATCCTAGGGACGAAATAGTTGTGAGGAGTAGAGATAAAGAAGAGGACTTAGTTAGTCTT	300
Db	1168	AACACTAAGGAAGAAGTAATTGTGAGGAGTAAAGACA---AAGAGGATTTAGTTTGTAGT	1224
Qy	301	AACATCCTTCATACTCAGCAGGAGTTATCTACAGTCCTTACGAAATCAGTTGAAGAAGAA	360
Db	1225	GCAGCCCTTCACAGTCCACAAGAATCACCT-----GTGGGTAAAGAA	1266
Qy	361	GATAGAGTTCTGTCTCCAGAAAAACAAAGGACAGTTTAAAGGAAAAGGGAGTTGCAGCA	420
Db	1267	GACAGAGTTGTGTCTCCAGAAAAGACAATGGACATTTTAAATGAAATGCAGATGTCAGTA	1326
Qy	421	GAAGCTTCTATGGGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTG	480
Db	1327	GTAGCACCTGTGAGGGAAGAGTATGCAGACTTTAAGCCATTTGAACAAGCATGGGAAGTG	1386
Qy	481	AAAGATACTTACAAGCAAGATAGTGATGTTTTGATTGCTGGAGGTAATATAGAGAGCAAA	540
Db	1387	AAAGATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCTAAT-----	1434
Qy	541	TTGGAAGGTAAAGTGGATAAGAAACACTTTTCAGATAGCCTTGAACAAACAAATCGTGAA	600
Db	1435	GTGGAAAGTAAAGTGGACAGAAAAATGCTTGGGAAGATAGCCTGGAGCAAAAAAGTCTTGGG	1494
Qy	601	AAAGATAGTGAAAGCAGTAATGATGACACTTCATTTCCAGTACACCAGAAGCTGTAAGA	660
Db	1495	AAGGATAGTGAAAGCAGAAATGAGGATGCTTCTTTCCCCAGTACCCCAAGCCTGTGAAG	1554
Qy	661	GGTGGTTCCGGAGCGTACATCACGTGTGCTCCCTTTAACCCAACAACAGAGAATGTTTCA	720
Db	1555	GACAGCTCCAGAGCATATATTACCTGTGCTTCCTTTACCTCAGCAACCGAAAGCACCACA	1614
Qy	721	ACAAACATTTTCCCTTGTTGGAAGATCATACTTCGGAAAATAAGACAGATGAAAAAAG	780
Db	1615	GCAAACACTTTCCCTTTGTTAGAAGATCATACTTCAGAAAATAAAACAGATGAAAAAAG	1674
Qy	781	ATAGAA-AAAAAAGGCACAAATTGTAACAGAGAAGAATGCAAGTGTCAAGACATCAAAC	839
Db	1675	ATAGAAGAAAGGAAGGCCCAAATTATAACAGAGAAGA---CTAGCCCCAAACGTCAAAT	1731
Qy	840	CCTTTCCTTATGGCAGCACAGGAGTCTAAGACAGATTACGTTACAACAGATCATGTGTCA	899
Db	1732	CCTTTCCTTGTAGCAGTACAGGATTCTGAGGCAGATTATGTTACAACAGATACCTTATCA	1791
Qy	900	AAGGTGACCGAGGAAGTAGTGGCAAACATGCCTGAAGGTCTAACCCAGATTTGGTTTCAG	959
Db	1792	AAGGTGACTGAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGCCAGATTTAGTTTCAG	1851

Qy 960 GAAGCATGTGAAAGTGAATTGAATGAAGCTACTGGTACAAAAATTGCCTTTGAAACAAA 1019
 |||
 Db 1852 GAAGCATGTGAAAGTGAAGTGAATGAAGCCACAGGTACAAAGATTGCTTATGAAACAAA 1911

Qy 1020 ATGGACCTGGTTCAAACCTCAGAAGCTGTGCAGGAGTCACTTTACCCTGTAACACAGCTT 1079
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 Db 1912 GTGGACTTGGTCCAAACATCAGAAGCTATACAAGAATCACTTTACCCACAGCACAGCTT 1971

Qy 1080 TGCCCATCTTTTGAAGAATCTGAAGCTACTCCGTCACCGGTTTTGCCTGACATTGTCATG 1139
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 Db 1972 TGCCCATCATTGAGGAAGCTGAAGCAACTCCGTCACCAGTTTTGCCTGATATTGTTATG 2031

Qy 1140 GAAGCACCATTAAATTCTGTAGTTCCTAGTGCTGGTGCTTCTGCAGTGCAGCTCAGTTCA 1199
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 Db 2032 GAAGCACCATTAAATTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAGTGCAGCCCAGTGTA 2091

Qy 1200 TCACCATTAGAACTCTTCCTTCAGTTAATTATGAAAGCATAAAGTTTGAGCCTGAAAAT 1259
 |||
 Db 2092 TCCCCACTGGAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGCTTGAGCCTGAAAAC 2151

Qy 1260 CCCCCACCATATGAGGAGGCCATGAATGTATCACTAAAAAAGAATCAGGAATGAATGAA 1319
 |||
 Db 2152 CCCCCACCATATGAAGAAGCCATGAATGTAGCACT---AAAAGCTTTGGGAACAAAGGAA 2208

Qy 1320 GAAATCACAGAGCCTGAAGGTATTAGTGTAGCTGTTTCAGGAAACAGAAGCTCCTTATATA 1379
 |||
 Db 2209 GGAATAAAAAGAGCCTGAAAGTTTAAATGCAGCTGTTTCAGGAAACAGAAGCTCCTTATATA 2268

Qy 1380 TCTATTGCATGTGATTTAATTAAAGAAACAAAGATCTCTACTGAACCGACTCCAGATTTT 1439
 |||
 Db 2269 TCCATTGCGTGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTTT 2328

Qy 1440 TCTAGTTATTCAGAAATAGCAGAAGTTGCACAGCCAGTGCCCGAGCATTCTGAGCTAGTT 1499
 |||
 Db 2329 TCTAATTATTCAGAAATAGCAAAATTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAGTG 2388

Qy 1500 GAAGATTCTCCCCGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCCGAA 1559
 |||
 Db 2389 GAGGATTCTCACCTGAATCTGAACCAGTTGACTTATTTAGTGATGATTGATTCTCTGAA 2448

Qy 1560 GTTCCACAAAAACAAGATGAAGCTGTAATACTTGTGAAAGAAAACCTCACTGAAATTTCA 1619
 |||
 Db 2449 GTCCACAAACACAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGAAGTGTC- 2507

Qy 1620 TCTGAGTCAATGACAGGACATGACAATAAGGGAAAACCTCAGTGCTTCACCATCACCTGAG 1679
 |||
 Db 2508 -----TGAGACAGTAGCCCAGCACAAAGAGGAGAGACTTAGTGCCTCAC---CTCAGGAG 2559

Qy 1680 GGAGGAAAACCGTATTTGGAGTCTTTTCAGCCCAGTTTAGGCATCACAAAAGATACCTTA 1739
 |||
 Db 2560 CTAGGAAAGCCATATTTAGAGTCTTTTCAGCCCAATTTACATAGTACAAAAGATGC---T 2616

Qy 1740 GCACCTGATGAAGTTTCAGCATTGACCCAAAAGGAGAAAATCCCTTTGCAGATGGAGGAG 1799
 |||
 Db 2617 GCATCTAATGACATTCCAACATTGACCAAAAAGGAGAAAATTTCTTTGCAAATGGAAGAG 2676

Qy 1800 CTCAATACTGCAGTTTATTCAAGTGATGGCTTATTCATTGCTCAGGAAGCAAACCTAAGA 1859

Db	2677	TTTAATACTGCAATTTATTCAAATGATGACTTACTTTCTTCTAAGGAAGACAAAATAAAA	2736
Qy	1860	GAAAGTGAAACATTTTCAGATTCATCTCCGATTGAGATTATAGATGAGTTCCCGACCTTT	1919
Db	2737	GAAAGTGAAACATTTTCAGATTCATCTCCGATTGAGATAATAGATGAATTTCCCACGTTT	2796
Qy	1920	GTCAGTTCTAAAGCAGATTCTTCTCCTACATTAGCCAGGGAATACACTGACCTAGAAGTA	1979
Db	2797	GTCAGTGCTAA---AGATGATTCTCCTAAATTAGCCAAGGAGTACACTGATCTAGAAGTA	2853
Qy	1980	GCCCACAAAAGTGAAATTGCTGACATCCAGGATGGAGCTGGGTTCATTGGCTTGTGCAGGA	2039
Db	2854	TCCGACAAAAGTGAAATTGCTAATATCCAAAGCGGGCAGATTTCATTGCCTTGCTTAGAA	2913
Qy	2040	TTGCCCATGACCTTTCTTTCAAGAGTATACAACCTAAAGAGGAAGTTCATGTCCAGAT	2099
Db	2914	TTGCCCTGTGACCTTTCTTTCAAGAATATATATCCTAAAGATGAAGTACATGTTTCAGAT	2973
Qy	2100	GAGTTCTCCAAAGATAGGGGTGATGTTTCAAAGGTGCCCGTACTGCCTCCAGATGTTTCT	2159
Db	2974	GAATTCTCCGAAAATAGGTCCAGTGATCTAAGGCATCCATATCGCCTTCAAATGTCTCT	3033
Qy	2160	GCTTTGGATGCTCAAGCAGAGATAGGCAGCATAGAAAAACCCAAAGTTCTTGTGAAAGAA	2219
Db	3034	GCTTTGGAACCTCAGACAGAAATGGGCAGCATAGTTAAATCCAAATCATTACGAAAGAA	3093
Qy	2220	GCCGAGAGAAAACTTCCTTCTGATACAGAAAAAGAGCGAAGATCTCCATCTGCTATATTT	2279
Db	3094	GCAGAGAAAAAACTTCCTTCTGACACAGAGAAAGAGGACAGATCCCTGTGAGCTGTATTG	3153
Qy	2280	TCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAGAAG	2339
Db	3154	TCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAGAAG	3213
Qy	2340	ACTGGAGTGGTGTGTTGGTGCCAGCTTGTTCCCTGCTGCTCTCGCTGACAGTATTCAGCATT	2399
Db	3214	ACTGGAGTGGTGTGTTGGTGCCAGCTTATTCCTGCTGCTGTCTCTGACAGTGTTCAGCATT	3273
Qy	2400	GTGAGTGTAAACGGCCTACATTGCCTTGCCCTGCTCTCTGTGACTATCAGCTTTAGGATA	2459
Db	3274	GTCAGTGTAAACGGCCTACATTGCCTTGCCCTGCTCTCGGTGACTATCAGCTTTAGGATA	3333
Qy	2460	TATAAGGGTGTGATCCAGGCTATCCAGAAATCTGATGAAGGCCACCCATTTCAGGGCATAT	2519
Db	3334	TATAAGGGCGTGATCCAGGCTATCCAGAAATCAGATGAAGGCCACCCATTTCAGGGCATAT	3393
Qy	2520	TTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGCAATTCTGCTCTT	2579
Db	3394	TTAGAATCTGAAGTTGCTATATCAGAGGAATTGGTTCAGAAATACAGTAATTCTGCTCTT	3453
Qy	2580	GGTCATGTAACTGCACAATAAAAGAACTCAGACGCCTCTTCTTAGTTGATGATTTAGTT	2639
Db	3454	GGTCATGTGAACAGCACAATAAAAGAACTGAGGCGGCTTTTCTTAGTTGATGATTTAGTT	3513
Qy	2640	GATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTCAAT	2699

Db 3514 GATTCCCTGAAGTTTGCAGTGTTGATGTGGGTGTTTACTTATGTTGGTGCCTTGTTCAAT 3573
 Qy 2700 GGTCTGACACTACTAATTTTGGCTCTGATTTCACTCTTCAGTGTTCTGTTATTTATGAA 2759
 |||||
 Db 3574 GGTCTGACACTACTGATTTTAGCTCTGATCTCACTCTTCAGTATTCTGTTATTTATGAA 3633
 Qy 2760 CGGCATCAGGCGCAAATAGATCATTATCTGGGACTTGCAAATAAGAATGTTAAAGATGCT 2819
 |||||
 Db 3634 CGGCATCAGGTGCAGATAGATCATTATCTAGGACTTGCAAACAAGAGTGTTAAGGATGCC 3693
 Qy 2820 ATGGCTAAAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGAATGAGAAAACCTG 2879
 |||||
 Db 3694 ATGGCCAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCAGATTGAAAAAGCCCC 3753
 Qy 2880 AAAGAGTTAACAATAGAGGAGTTTATCTTTAAAGGGGATATTCATTTGATTCCATTGGGG 2939
 . ||
 Db 3754 AA-----ACAGAAGTTCATCTTTAAAGGGGACACTCACTTGATTAC----GGG 3797
 Qy 2940 AGGGTCAGGGAAGAACAAGCCCTTGACATTGCAGTGCAGTTTCACAGATCTTTATTTTTA 2999
 || |||||
 Db 3798 GGTGGGAGGGTCAGGGGTGAGCCCTTGGTGGCCGTGCGGTTT--CAGCTCTTTATTTTTA 3855
 Qy 3000 GCAACGCAGTGTCTGAGGAAAAATGACCTGTCTTGACTGCCCTGTGTTTCATCATCTTAAG 3059
 ||| ||| |||
 Db 3856 GCAGTGCAGTGTCTGAGGAAAAATTACCTGTCTTGACTT-CCTGTGTTTATCATCTTAAG 3914
 Qy 3060 TATTGTAAGCTGCTATGTATGGATTTAAATCGTAATCATATTTGTTTTTCTGTATGAGG 3119
 |||||
 Db 3915 TATTGTAAGCTGCTGTGTATGGATCT-CATTGTAGTCACACTTGTCTTCCCAATGAGGC 3973
 Qy 3120 CACTGGTGAATAAAACAAAGATCTGAGAAAGCTGTATATTACACTTTGTGCGAGGTAGTCT 3179
 |||||
 Db 3974 GCCTGGTGAATAAAGGA--CTCGGGGAAAGCTGTGCATTGTATCTGCTGCAGGGTAGTCT 4031
 Qy 3180 TGCTGTATTTGGGGAATTGCAAAGAAAGTGGAGCT---GACAGAAATAACCCCTTTTCACA 3236
 |||||
 Db 4032 AGCTGTATGCAGAGAGTTGTAAAGAAGGCAAATCTGGGGGCAGGGAAAACCCCTTTTCACA 4091
 Qy 3237 GTTTGTGCACTGTGTACGGTCTGTGTAGGTTGATGCAGATTTTCTGAAATGAAATGTTTA 3296
 | ||| | ||| | ||| |
 Db 4092 G--TGACTGTGTTTGGTCAGTGTAAACTGATGCAGATTTTCTGAAATGAAATGTTTA 4149
 Qy 3297 GACGAGATCATGCCACCAAGGCAGGAGTGAAAAAGCTTGCCTTTCTGGTATGTTCTAGG 3356
 || ||||| ||| | ||| |||||
 Db 4150 GATGAGAGCATACTACTAAAGCAGAGTGGAATACTCTGTC--TTTATGGTGTGTTCTAGG 4207
 Qy 3357 TGTATTGTGAAATTTACTGTTGTATTAATTGCCAATATAAGTAAATATAGATTATATATA 3416
 |||||
 Db 4208 TGTATTGTG-AATTTACTGTTATATT---GCCAATATAAGTAAATATAGA---CCTAA 4258
 Qy 3417 TCTATATATAGTGTTCACGAAGCTTAGCCCTTTACCTTCCCAGCTGCCCCACAGTGCTT 3476
 |||||
 Db 4259 TCTATATATAGTGTTCACAAAGCTTAGATCTTTAACCTTGACAGCTGCCCCACAGTGCTT 4318
 Qy 3477 GATACTTCTGTCATGGGTTTTATGTGTGTAGTCCCAAAGCACATAAGCTAGGGAGAAACG 3536
 || | ||||| |||||
 Db 4319 GACCTCTGAGTCATTGGTTATGCAGTGTAGTCCCAAAGCACATAAACTAGGAAGAGAAATG 4378

Qy 3537 TACTTCTAGGCGCACTACC-ATCTGTTTTCAACACGAACCGACGCCATGCAAACAGAACT 3595
 || || |||| | |||| | | | | || || | | |||| || |
 Db 4379 TATTTGTAGGAGTGCTACCTACCACCTGTTTTCAAGAAAATATAGAACTCCAACAAAAAT 4438
 Qy 3596 CCTCAACATAAACTTCACTGCACAGACTTACTGTAGTTAATTTTATCACAAACTC----- 3650
 || | | | | | | | | | | |||| |||| ||||
 Db 4439 ATAGAATGTCATTTCAAAGACTTACTGTATGTATAGTTAATTTTGTACAGACTCTGAAA 4498
 Qy 3651 -----TGGACTGAATCTAATGCTTCCAAAAATGTTTGCAAATATCAAACATTGTTATGTA 3705
 |||| |||| | |||| |||| |||| |||| |||| |||| ||||
 Db 4499 TTCTATGGACTGAATTTTCATGCTTCC--AAATGTTTGCAGTTATCAAACATTGTTATGCA 4556
 Qy 3706 AGAAAATAT-AAATGACGATTTATACAATTGTGGTTTAAGCTGTATTGAACTAAATCTGT 3764
 |||| | | |||| | | |||| |||| |||| |||| |||| ||||
 Db 4557 AGAAATCATAAAATGAAGACTTATACCATTGTGGTTTAAGCCGTACTGAATT--ATCTGT 4614
 Qy 3765 GGAATGCATTGTGAACTGTAAAAGCAAAGTATCAATAAAGCTTATAGACTTAAAAAAAAA 3824
 |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
 Db 4615 GGAATGCATTGTGAACTGTAAAAGCAAAGTATCAATAAAGCTTATAGACTTAAAAAAAAA 4674
 Qy 3825 AAAAAAAAA 3833
 |||| ||||
 Db 4675 AAAAAAAAA 4683

RESULT 13

ABN86600

ID ABN86600 standard; DNA; 4684 BP.

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AC ABN86600;

XX

DT 05-NOV-2002 (first entry)

XX

DE Rat neurotransmitter receptor protein Nogo encoding DNA.

XX

KW Nerve regeneration; neuroprotection; neuronal degeneration; CNS; PNS;
 KW central nervous system; peripheral nervous system; tranquillizer; Nogo;
 KW vulnerary; cerebroprotective; anti-tumour; antidiabetic; anticonvulsant;
 KW nootropic; antiparkinsonian; ophthalmological; analgesic; hepatotropic;
 KW osteopathic; vasotropic; nephrotropic; cytostatic; antigen; gene therapy;
 KW neurotransmitter receptor; rat; gene; ds.

XX

OS Rattus norvegicus.

XX

FH Key Location/Qualifiers

FT CDS 253. .3744

FT /*tag= a

FT /product= "Nogo-A"

XX

PN US2002072493-A1.

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PD 13-JUN-2002.

XX

PF 28-JUN-2001; 2001US-00893348.

XX

PR 19-MAY-1998; 98IL-00124500.

PR 21-JUL-1998; 98WO-US014715.
PR 22-DEC-1998; 98US-00218277.
PR 19-MAY-1999; 99US-00314161.

XX

PA (YEDA) YEDA RES & DEV CO LTD.

XX

PI Eisenbach-Schwartz M, Hauben E, Cohen IR, Beserman P, Mosonego A;
PI Moalem G;

XX

DR WPI; 2002-607255/65.

DR P-PSDB; ABB81074, ABB81076, ABB81077.

XX

PT Promoting nerve regeneration and preventing neuronal degeneration in the
PT central/peripheral nervous system from injury/disease, comprises
PT administering nervous system-specific activated T cells/antigen, or
PT analogs/peptides.

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PS Disclosure; Page 40-44; 93pp; English.

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CC The invention relates to promoting nerve regeneration or conferring
CC neuroprotection and preventing or inhibiting neuronal degeneration in the
CC central/peripheral nervous system (NS). The method involves administering
CC NS-specific activated T cells, NS-specific antigen, its analogue or its
CC peptide, a nucleotide sequence the NS-specific antigen or its analogue or
CC combinations. The method is useful for promoting nerve regeneration and
CC preventing neuronal degeneration in central/peripheral nervous system
CC from injury/disease, where the injury is spinal cord injury, blunt
CC trauma, penetrating trauma, hemorrhagic stroke, ischaemic stroke or
CC damages caused by surgery such as tumour excision. The disease is not an
CC autoimmune disease or neoplasm. The disease results in a degenerative
CC process occurring in either gray or white matter or both. The disease is
CC diabetic neuropathy, senile dementia, Alzheimer's disease, Parkinson's
CC disease, facial nerve (Bell's) palsy, glaucoma, Huntington's chorea,
CC amyotrophic lateral sclerosis, non-arteritic optic neuropathy, and
CC vitamin deficiency, intervertebral disc herniation, prion diseases such
CC as Creutzfeldt-Jakob disease, carpal tunnel syndrome, peripheral
CC neuropathies associated with various diseases, including but not limited
CC to uremia, porphyria, hypoglycemia, Sjorgren Larsson syndrome, acute
CC sensory neuropathy, chronic ataxic neuropathy, biliary cirrhosis, primary
CC amyloidosis, obstructive lung diseases, acromegaly, malabsorption
CC syndromes, polycythemia vera, immunoglobulin (Ig)A- and IgG gamma-
CC pathies, complications of various drugs (e.g., metronidazole) and toxins
CC (e.g., alcohol or organophosphates), Charcot-Marie-Tooth disease, ataxia
CC telangiectasia, Friedreich's ataxia, amyloid polyneuropathies,
CC adrenomyeloneuropathy, Giant axonal neuropathy, Refsum's disease, Fabry's
CC disease, or lipoproteinemia. The present sequence represents a DNA
CC encoding the rat neurotransmitter receptor protein Nogo (Nogo-A, Nogo-B
CC and Nogo-C), an example of NS-specific antigen

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SQ Sequence 4684 BP; 1358 A; 1047 C; 1112 G; 1167 T; 0 U; 0 Other;

Query Match 56.9%; Score 2179.4; DB 6; Length 4684;
Best Local Similarity 78.2%; Pred. No. 0;
Matches 3008; Conservative 0; Mismatches 731; Indels 110; Gaps 28;

Qy 1 CTATCTCCTCTCTCAGCCGCTGCTTTTAAAGAACGTGAATACCTTGGTGATTTACCAGCA 60
|||||

Db 928 CTATCTCCTCTCTCAACTGTTTCTTTTAAAGAACATGGATACCTTGGTAACTTATCAGCA 987

Qy 61 GTACTGCCCCACTGAAGGAACACTTCCAGCAACTTCAAATGAAGCTTCTAAAGCATTCTCA 120
 || || | ||||| || || |||| | ||||| ||||| || ||

Db 988 GTGTCATCCTCAGAAGGAACAATTGAAGAACTTTAAATGAAGCTTCTAAAGAGTTGCCA 1047

Qy 121 GAGAAGGCCAAAAATCCATTTGTAGAGAGAAATTTAACAGAATTTTCAGAATTGGAATAT 180
 |||| | |||| | ||||| || || |||| | ||||| |||||

Db 1048 GAGAGGGCAACAAATCCATTTGTAAATAGAGATTTAGCAGAATTTTCAGAATTAGAATAT 1107

Qy 181 TCAGAAATGGAATCATCATTCAGTGGCTCTCAAAAGGCAGAACCTGCCGTAACAGTAGCG 240
 ||||| ||||| || | |||| | || | || | || | || ||||

Db 1108 TCAGAAATGGGATCATCTTTTAAAGGCTCCCCAAAAGGAGAGTCAGCCATATTAGTAGAA 1167

Qy 241 AATCCTAGGGACGAAATAGTTGTGAGGAGTAGAGATAAAGAAGAGGACTTAGTTAGTCTT 300
 || ||| ||| ||| || ||||| ||||| || | ||||| ||||| || |

Db 1168 AACACTAAGGAAGAAGTAATTGTGAGGAGTAAAGACA---AAGAGGATTTAGTTTGTAGT 1224

Qy 301 AACATCCTTCATACTCAGCAGGAGTTATCTACAGTCCTTACGAAATCAGTTGAAGAAGAA 360
 ||||| | || || | || | || || || || ||||

Db 1225 GCAGCCCTTCACAGTCCACAAGAATCACCT-----GTGGGTAAAGAA 1266

Qy 361 GATAGAGTTCTGTCTCCAGAAAAACAAAGGACAGTTTAAAGGAAAAGGGAGTTGCAGCA 420
 || ||||| ||||| ||||| |||| | |||| | |||| | |||| |

Db 1267 GACAGAGTTGTGTCTCCAGAAAAGACAATGGACATTTTAAATGAAATGCAGATGTCAGTA 1326

Qy 421 GAAGCTTCTATGGGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTG 480
 | ||| || || |||| || ||||| ||||| || ||||| || ||||| |||||

Db 1327 GTAGCACCTGTGAGGGAAGAGTATGCAGACTTTAAGCCATTTGAACAAGCATGGGAAGTG 1386

Qy 481 AAAGATACTTACAAGCAAGATAGTGATGTTTTGATTGCTGGAGGTAATATAGAGAGCAAA 540
 ||||| |||| | || | |||| || || |||| ||| ||||

Db 1387 AAAGATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCTAAT----- 1434

Qy 541 TTGGAAGGTAAAGTGGATAAGAAACACTTTTCAGATAGCCTTGAACAAACAAATCGTGAA 600
 |||| | ||||| || | ||| || | ||||| || |||| | || ||

Db 1435 GTGGAAAGTAAAGTGGACAGAAAATGCTTGGAAAGATAGCCTGGAGCAAAAAGTCTTGGG 1494

Qy 601 AAAGATAGTGAAAGCAGTAATGATGACACTTCATTTCCCAGTACACCAGAAGCTGTAAGA 660
 || ||||| |||| |||| || || || || ||||| ||||| |||| |

Db 1495 AAGGATAGTGAAGGCAGAAATGAGGATGCTTCTTTCCCCAGTACCCCAGAACCTGTGAAG 1554

Qy 661 GGTGGTTCCGGAGCGTACATCACGTGTGCTCCCTTTAACCCAACAACTGAGAATGTTTCA 720
 | | ||| |||| || || || ||||| ||||| | || |||| || | ||

Db 1555 GACAGCTCCAGAGCATATATTACCTGTGCTTCCTTTACCTCAGCAACCGAAAGCACCACA 1614

Qy 721 ACAAACATTTTCCCTTGTTGGAAGATCATACTTCGGAAAATAAGACAGATGAAAAAAG 780
 ||||| ||| || |||| | ||||| ||||| ||||| ||||| |||||

Db 1615 GCAAACACTTTCCTTTGTTAGAAGATCATACTTCAGAAAATAAAACAGATGAAAAAAA 1674

Qy 781 ATAGAA-AAAAAAGGCACAAATTGTAACAGAGAAGAATGCAAGTGTCAAGACATCAAAC 839
 ||||| ||| |||| | |||| | ||||| || || |||| | ||||

Db 1675 ATAGAAGAAAGGAAGGCCCAAATTATAACAGAGAAGA---CTAGCCCCAAAACGTCAAAT 1731

Qy 840 CCTTTCCTTATGGCAGCACAGGAGTCTAAGACAGATTACGTTACAACAGATCATGTGTCA 899
 ||||| || | |||| | |||| || || ||||| ||||| || ||||

Db 1732 CCTTTCCTTGTAGCAGTACAGGATTCTGAGGCAGATTATGTTACAACAGATACCTTATCA 1791

Qy 900 AAGGTGACCGAGGAAGTAGTGGCAAACATGCCTGAAGGTCTAACCCAGATTTGGTTCAG 959
 ||||| ||| || ||| ||||| ||||| ||| ||||| |||||
 Db 1792 AAGGTGACTGAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGCCAGATTTAGTTCAG 1851

Qy 960 GAAGCATGTGAAAGTGAATTGAATGAAGCTACTGGTACAAAAATTGCCTTTGAAACAAAA 1019
 ||||| ||||| ||||| ||| ||||| ||||| ||| ||||| |||||
 Db 1852 GAAGCATGTGAAAGTGAAGTGAATGAAGCCACAGGTACAAAGATTGCTTATGAAACAAAA 1911

Qy 1020 ATGGACCTGGTTCAAACCTCAGAAGCTGTGCAGGAGTCACTTTACCCTGTAACACAGCTT 1079
 ||||| ||||| ||||| ||||| ||| ||| ||||| ||||| ||| |||||
 Db 1912 GTGGACTTGGTCCAAACATCAGAAGCTATACAAGAATCACTTTACCCACAGCACAGCTT 1971

Qy 1080 TGCCCATCTTTGAAGAATCTGAAGCTACTCCGTCACCGGTTTTGCCTGACATTGTCATG 1139
 ||||| ||||| ||| ||||| ||||| ||||| ||||| ||||| |||
 Db 1972 TGCCCATCATTGAGGAAGCTGAAGCAACTCCGTCACCAGTTTTGCCTGATATTGTTATG 2031

Qy 1140 GAAGCACCATTAAATTCTGTAGTTCCTAGTGCTGGTGCTTCTGCAGTGCAGCTCAGTTCA 1199
 ||||| ||||| ||| ||| ||| ||| ||||| ||||| ||||| |||
 Db 2032 GAAGCACCATTAAATTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAGTGCAGCCAGTGTA 2091

Qy 1200 TCACCATTAGAACTCTTCCTTCAGTTAATTATGAAAGCATAAAGTTTGAGCCTGAAAAAT 1259
 || ||| ||| ||| ||| ||||| ||||| ||| ||||| ||||| |||||
 Db 2092 TCCCCACTGGAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGCTTGAGCCTGAAAAC 2151

Qy 1260 CCCCCACCATATGAGGAGGCCATGAATGTATCACTAAAAAAGAATCAGGAATGAATGAA 1319
 ||||| ||||| ||| ||||| ||||| ||||| ||||| ||| |||||
 Db 2152 CCCCCACCATATGAAGAAGCCATGAATGTAGCACT---AAAAGCTTTGGGAACAAAGGAA 2208

Qy 1320 GAAATCACAGAGCCTGAAGGTATTAGTGTAGCTGTTTCAGGAAACAGAAGCTCCTTATATA 1379
 | ||| | ||||| || ||| || ||||| ||||| ||||| ||||| |||||
 Db 2209 GGAATAAAAGAGCCTGAAAGTTTAAATGCAGCTGTTTCAGGAAACAGAAGCTCCTTATATA 2268

Qy 1380 TCTATTGCATGTGATTTAATTAAAGAAACAAAGATCTCTACTGAACCGACTCCAGATTTTC 1439
 || ||||| ||||| ||||| ||||| ||||| ||||| ||| ||||| |||||
 Db 2269 TCCATTGCGTGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTTTC 2328

Qy 1440 TCTAGTTATTCAGAAATAGCAGAAGTTGCACAGCCAGTGCCCGAGCATTCTGAGCTAGTT 1499
 ||||| ||||| ||||| ||| ||| ||| ||||| ||| ||||| |||||
 Db 2329 TCTAATTATTCAGAAATAGCAAAATTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAGTG 2388

Qy 1500 GAAGATTCCCTCCCCCGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCCGAA 1559
 || ||||| || ||| ||||| ||||| ||||| ||||| ||| |||||
 Db 2389 GAGGATTCCCTCACCTGAATCTGAACCAGTTGACTTATTTAGTGATGATTGATTTCCTGAA 2448

Qy 1560 GTTCCACAAAAACAAGATGAAGCTGTAATACTTGTGAAAGAAAACCTCACTGAAATTTCA 1619
 || ||||| ||||| || ||||| || ||| ||||| ||| ||||| |||||
 Db 2449 GTCCACAAACACAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGAAGTGTC- 2507

Qy 1620 TCTGAGTCAATGACAGGACATGACAATAAGGGAAAACCTCAGTGCTTCACCATCACCTGAG 1679
 | || ||| ||| ||| ||| ||||| ||||| ||||| ||| |||||
 Db 2508 -----TGAGACAGTAGCCCAGCACAAAGAGGAGAGACTTAGTGCCTCAC---CTCAGGAG 2559

Qy 1680 GGAGGAAAACCGTATTTGGAGTCTTTTCAGCCCAGTTTAGGCATCACAAAGATACCTTA 1739
 ||||| || ||||| ||||| ||||| ||||| ||||| ||| ||||| |||||
 Db 2560 CTAGGAAAGCCATATTTAGAGTCTTTTCAGCCCAATTTACATAGTACAAAGATGC---T 2616

Qy	1740	GCACCTGATGAAGTTTCAGCATTGACCCAAAAGGAGAAAATCCCTTTGCAGATGGAGGAG	1799
Db	2617	GCATCTAATGACATTCCAACATTGACCAAAAAGGAGAAAATTTCTTTGCAAATGGAAGAG	2676
Qy	1800	CTCAATACTGCAGTTTATTCAAGTGATGGCTTATTCATTGCTCAGGAAGCAAACCTAAGA	1859
Db	2677	TTTAATACTGCAATTTATTCAAATGATGACTTACTTTCTTCTAAGGAAGACAAAATAAAA	2736
Qy	1860	GAAAGTGAAACATTTTCAGATTTCATCTCCGATTGAGATTATAGATGAGTTCCCGACCTTT	1919
Db	2737	GAAAGTGAAACATTTTCAGATTTCATCTCCGATTGAGATAATAGATGAATTTCCCACGTTT	2796
Qy	1920	GTCAGTTCTAAAGCAGATTCTTCTCCTACATTAGCCAGGGAATACACTGACCTAGAAGTA	1979
Db	2797	GTCAGTGCTAA---AGATGATTCTCCTAAATTAGCCAAGGAGTACACTGATCTAGAAGTA	2853
Qy	1980	GCCCACAAAAGTGAAATTGCTGACATCCAGGATGGAGCTGGGTCATTGGCTTGTGCAGGA	2039
Db	2854	TCCGACAAAAGTGAAATTGCTAATATCCAAAAGCGGGCAGATTCAATTGCCTTGCTTAGAA	2913
Qy	2040	TTGCCCATGACCTTTCTTTCAAGAGTATACAACCTAAAGAGGAAGTTCATGTCCAGAT	2099
Db	2914	TTGCCCTGTGACCTTTCTTTCAAGAATATATATCCTAAAGATGAAGTACATGTTTCAGAT	2973
Qy	2100	GAGTTCTCCAAAGATAGGGGTGATGTTTCAAAGGTGCCCCGACTGCCTCCAGATGTTTCT	2159
Db	2974	GAATTCTCCGAAAATAGGTCCAGTGTATCTAAGGCATCCATATCGCCTTCAAATGTCTCT	3033
Qy	2160	GCTTTGGATGCTCAAGCAGAGATAGGCAGCATAGAAAAACCCAAAGTTCTTGTGAAAGAA	2219
Db	3034	GCTTTGGAACCTCAGACAGAAATGGGCAGCATAGTTAAATCCAAATCACTTACGAAAGAA	3093
Qy	2220	GCCGAGAGAAAACCTTCCTTCTGATACAGAAAAAGAGCGAAGATCTCCATCTGCTATATTT	2279
Db	3094	GCAGAGAAAAAACTTCCTTCTGACACAGAGAAAGAGGACAGATCCCTGTGAGCTGTATTG	3153
Qy	2280	TCAGCAGAGCTGAGTAAAACCTTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAGAAG	2339
Db	3154	TCAGCAGAGCTGAGTAAAACCTTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAGAAG	3213
Qy	2340	ACTGGAGTGGTGTGTTGGTGCCAGCTTGTTCTGCTGCTCTCGCTGACAGTATTCAGCATT	2399
Db	3214	ACTGGAGTGGTGTGTTGGTGCCAGCTTATTCCTGCTGCTGTCTCTGACAGTGTTCAGCATT	3273
Qy	2400	GTGAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATA	2459
Db	3274	GTCAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCGGTGACTATCAGCTTTAGGATA	3333
Qy	2460	TATAAGGGTGTGATCCAGGCTATCCAGAAATCTGATGAAGGCCACCCATTACAGGGCATAT	2519
Db	3334	TATAAGGGCGTGATCCAGGCTATCCAGAAATCAGATGAAGGCCACCCATTACAGGGCATAT	3393
Qy	2520	TTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGCAATTCTGCTCTT	2579
Db	3394	TTAGAATCTGAAGTTGCTATATCAGAGGAATTGGTTCAGAAATACAGTAATTCTGCTCTT	3453
Qy	2580	GGTCATGTAACTGCACAATAAAAGAACTCAGACGCCTCTTCTTAGTTGATGATTTAGTT	2639

Db	3454	GGTCATGTGAACAGCACAAATAAAAGAACTGAGGCGGCTTTTCTTAGTTGATGATTTAGTT	3513
Qy	2640	GATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTCAAT	2699
Db	3514	GATTCCCTGAAGTTTGCAGTGTTGATGTGGGTGTTTACTTATGTTGGTGCCTTGTTCAAT	3573
Qy	2700	GGTCTGACACTACTAATTTTGGCTCTGATTTCACTCTTCAGTGTTCCCTGTTATTTATGAA	2759
Db	3574	GGTCTGACACTACTGATTTTAGCTCTGATCTCACTCTTCAGTATTCCTGTTATTTATGAA	3633
Qy	2760	CGGCATCAGGCGCAAATAGATCATTATCTGGGACTTGCAAATAAGAATGTTAAAGATGCT	2819
Db	3634	CGGCATCAGGTGCAGATAGATCATTATCTAGGACTTGCAAACAAGAGTGTTAAGGATGCC	3693
Qy	2820	ATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGAATGAGAAAGCCTG	2879
Db	3694	ATGGCCAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCAGATTGAAAAAGCCCC	3753
Qy	2880	AAAGAGTTAACAATAGAGGAGTTTATCTTTAAAGGGGATATTCATTTGATCCATTGGGG	2939
Db	3754	AA-----ACAGAAGTTCATCTTTAAAGGGGACACTCACTTGATTAC----GGG	3797
Qy	2940	AGGGTCAGGGAAGAACAAAGCCTTGACATTGCAGTGCAGTTTCACAGATCTTTATTTT	2999
Db	3798	GGTGGGAGGGTCAGGGGTGAGCCCTTGGTGCCGTGCGGTTT--CAGCTCTTTATTTT	3855
Qy	3000	GCAACGCAGTGTCTGAGGAAAAATGACCTGTCTTGACTGCCCTGTGTTTCATCATCTTAAG	3059
Db	3856	GCAGTGCAGTGTCTGAGGAAAAATTACCTGTCTTGACTT-CCTGTGTTTATCATCTTAAG	3914
Qy	3060	TATTGTAAGCTGCTATGTATGGATTTAAATCGTAATCATATTTGTTTTCTGTATGAGG	3119
Db	3915	TATTGTAAGCTGCTGTGTATGGATCT-CATTGTAGTCACACTTGCTCTCCCAATGAGGC	3973
Qy	3120	CACTGGTGAATAAACAAAGATCTGAGAAAGCTGTATATTACACTTTGTGCGCAGGTAGTCT	3179
Db	3974	GCCTGGTGAATAAAGGA--CTCGGGGAAAGCTGTGCATTGTATCTGCTGCAGGGTAGTCT	4031
Qy	3180	TGCTGTATTTGGGGAATTGCAAAGAAAGTGGAGCT---GACAGAAATAACCCTTTTCACA	3236
Db	4032	AGCTGTATGCAGAGAGTTGTAAAGAAGGCAAATCTGGGGGCAGGGAAAACCCTTTTCACA	4091
Qy	3237	GTTTGTGCACTGTGTACGGTCTGTGTAGGTTGATGCAGATTTTCTGAAATGAAATGTTTA	3296
Db	4092	G--TGTAAGTGTGTTGGTTCAGTGTAAACTGATGCAGATTTTCTGAAATGAAATGTTTA	4149
Qy	3297	GACGAGATCATGCCACCAAGGCAGGAGTGAAAAAGCTTGCCCTTTCCTGGTATGTTCTAGG	3356
Db	4150	GATGAGAGCATACTACTAAAGCAGAGTGAAAAACTCTGTC--TTTATGGTGTGTTCTAGG	4207
Qy	3357	TGTATTGTGAAATTTACTGTTGTATTAATTGCCAATATAAGTAAATATAGATTATATATA	3416
Db	4208	TGTATTGTG-AATTTACTGTTATAT----TGCCAATATAAGTAAATATAGA----CCTAA	4258
Qy	3417	TCTATATATAGTGTTTTCACGAAGCTTAGCCCTTTACCTTCCCAGCTGCCCCACAGTGCTT	3476

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Db      4259 TCTATATATAGTGTTCACAAAGCTTAGATCTTTAACCTTGCAGCTGCCCCACAGTGCTT 4318
Qy      3477 GATACTTCTGTCATGGGTTTTATGTGTGTAGTCCCAAAGCACATAAGCTAGGGAGAAACG 3536
      || | |||| ||| | ||||| | || | ||||| |
Db      4319 GACCTCTGAGTCATTGGTTAT-GCAGTGTAGTCCAAGCACATAAACTAGGAAGAGAAATG 4377
Qy      3537 TACTTCTAGGCGCACTACC-ATCTGTTTTCAACACGAACCGACGCCATGCAAACAGAACT 3595
      || || |||| | |||| | | | || || | | |||| || |
Db      4378 TATTTGTAGGAGTGCTACCTACCACCTGTTTTCAAGAAAATATAGAACTCCAACAAAAAT 4437
Qy      3596 CCTCAACATAAACTTCACTGCACAGACTTACTGTAGTTAATTTTATCACAAACTC----- 3650
      || | | | | | | | | ||||| |||| ||||
Db      4438 ATAGAATGTCATTTCAAAGACTTACTGTATGTATAGTTAATTTTGTACAGACTCTGAAA 4497
Qy      3651 -----TGGACTGAATCTAATGCTTCCAAAAATGTTTGCAAATATCAAACATTGTTATGTA 3705
      ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      4498 TTCTATGGACTGAATTCATGCTTCC--AAATGTTTGCAGTTATCAAACATTGTTATGCA 4555
Qy      3706 AGAAAATAT-AAATGACGATTTATACAATTGTGGTTTAAGCTGTATTGAACTAAATCTGT 3764
      |||| | ||||| || ||||| ||||| ||||| ||||| |||||
Db      4556 AGAAATCATAAAATGAAGACTTATACCATTGTGGTTTAAGCCGTAAGTT--ATCTGT 4613
Qy      3765 GGAATGCATTGTGAACTGTAAAAGCAAAGTATCAATAAAGCTTATAGACTTAAAAAAAAA 3824
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      4614 GGAATGCATTGTGAACTGTAAAAGCAAAGTATCAATAAAGCTTATAGATCTTAAAAAAAAA 4673
Qy      3825 AAAAAAAAA 3833
      |||||
Db      4674 AAAAAAAAA 4682

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RESULT 14

AAV30920

ID AAV30920 standard; cDNA; 2386 BP.

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AC AAV30920;

XX

DT 14-SEP-1998 (first entry)

XX

DE Human secreted protein BG160_1 cDNA.

XX

KW BG160_1; secreted protein; protein factor; human; ds.

XX

OS Homo sapiens.

XX

FH	Key	Location/Qualifiers
----	-----	---------------------

FT	CDS	102. .2030
----	-----	------------

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FT	sig_peptide	1863. .1899
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FT		/*tag= b
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FT		/note= "putative leader/signal peptide"
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FT	mat_peptide	1900. .2027
----	-------------	-------------

FT		/*tag= c
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XX

PN WO9817687-A2.

XX

PD 30-APR-1998.

XX
 PF 24-OCT-1997; 97WO-US019590.
 XX
 PR 25-OCT-1996; 96US-00740274.
 PR 24-OCT-1997; 97US-00740274.
 XX
 PA (GEMY) GENETICS INST INC.
 XX
 PI Jacobs K, Mccoy JM, Lavallie ER, Racie LA, Merberg D, Treacy M;
 PI Spaulding V, Agostino MJ;
 XX
 DR WPI; 1998-261426/23.
 DR P-PSDB; AAW58383.
 XX
 PT Nucleic acid encoding secreted protein from human cells - useful, e.g. as
 PT immuno-modulators, anti-tumour agents, promoters of tissue growth,
 PT haemostatic and thrombolytic agents etc.
 XX
 PS Claim 20; Page 74-75; 114pp; English.
 XX
 CC This cDNA clone, designated BG160_1, codes for a novel human secreted
 CC protein (see AAW58383). It was isolated from a human adult brain cDNA
 CC library using methods selective for cDNAs that encode secreted proteins.
 CC The clone is deposited in composite clone ATCC 98232; an oligonucleotide
 CC (see AAT99725) is designed to isolate the clone from the composite. The
 CC predicted AT415_4 amino acid sequence shows homology to neuroendocrine-
 CC specific proteins. Novel cDNA clones (see AAV30916-32) coding for human
 CC secreted proteins (see AAW58580-90) are claimed. These can be used for
 CC recombinant production of the secreted proteins for analysis,
 CC characterisation, diagnostic or therapeutic use. They can also be used as
 CC tissue or mol.wt. markers, for chromosome identification, to identify
 CC genetic disorders, to isolate new related DNA, as sources of primers for
 CC PCR, to generate antibodies, and in interaction trap assays. The secreted
 CC proteins may also have many biological activities, e.g. cytokine,
 CC immunomodulator, haematopoiesis regulating activity, tissue growth
 CC activity, activin or inhibin activity, chemotactic or chemokinetic
 CC activity, haemostatic and thrombolytic activity, receptor/ligand
 CC activity, antiinflammatory, cadherin and tumour invasion suppressor
 CC activity, and tumour inhibition activity. The proteins can be expressed
 CC in vivo from DNA, introduced in gene therapy vectors
 XX
 SQ Sequence 2386 BP; 756 A; 450 C; 494 G; 686 T; 0 U; 0 Other;

Query Match 46.4%; Score 1777.2; DB 2; Length 2386;
 Best Local Similarity 86.9%; Pred. No. 0;
 Matches 2101; Conservative 0; Mismatches 258; Indels 59; Gaps 11;

Qy 827 CAAGACATCAAACCCTTTCTTATGGCAGCACAGGAGTCTAAGACAGATTACGTTACAAC 886
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 Db 2 CAAAACATCAAACCCTTTCTTGTAGCAGCACAGGATTCTGAGACAGATTATGTCACAAC 61
 Qy 887 AGATCATGTGTCAAAGGTGACCGAGGAAGTAGTGGCAAACATGCCTGAAGGTCTAACCCC 946
 |||| || | ||||||||| ||||||| ||||||||||||||||||||| || || ||
 Db 62 AGATAATTTAACAAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCC 121
 Qy 947 AGATTTGGTTCAGGAAGCATGTGAAAGTGAATTGAATGAAGCTACTGGTACAAAAATTGC 1006
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Db	122	AGATTTAGTACAGGAAGCATGTGAAAGTGAAATTGAATGAAGTTACTGGTACAAAGATTGC	181
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Db	182	TTATGAAACAAAAATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCC	241
Qy	1067	TGTAACACAGCTTTGCCCATCTTTGAAGAATCTGAAGCTACTCCGTCACCGGTTTTGCC	1126
Db	242	TGCAGCACAGCTTTGCCCATCATTTGAAGAGTCAGAAGCTACTCCTTCACCAGTTTTGCC	301
Qy	1127	TGACATTGTCATGGAAGCACCATTAAATTCTGTAGTTCCTAGTGCTGGTGCTTCTGCAGT	1186
Db	302	TGACATTGTTATGGAAGCACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGAT	361
Qy	1187	GCAGCTCAGTTCATCACCATTAGAAACTCTTCCTTCAGTTAATTATGAAAGCATAAAGTT	1246
Db	362	ACAGCCCAGCTCATCACCATTAGAAGC---TTCTTCAGTTAATTATGAAAGCATAAAACA	418
Qy	1247	TGAGCCTGAAAAATCCCCACCATATGAGGAGGCCATGAATGTATCACTAAAAAAGAATC	1306
Db	419	TGAGCCTGAAAACCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAGTATC	478
Qy	1307	AGGAATGAATGAAGAAATCACAGAGCCTGAAGGTATTAGTGTAGCTGTTTCAGGAAACAGA	1366
Db	479	AGGAATAAAGGAAGAAATTAAGAGCCTGAAAATATTAATGCAGCTCTTCAAGAAACAGA	538
Qy	1367	AGCTCCTTATATATCTATTGCATGTGATTTAATTAAAGAAACAAAGATCTCTACTGAACC	1426
Db	539	AGCTCCTTATATATCTATTGCATGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAACC	598
Qy	1427	GACTCCAGATTTCTCTAGTTATTTCAGAAATAGCAGAAGTTGCACAGCCAGTGCCCGAGCA	1486
Db	599	AGCTCCGATTTCTCTGATTATTTCAGAAATGGCAAAGTTGAACAGCCAGTGCCCTGATCA	658
Qy	1487	TTCTGAGCTAGTTGAAGATTCCCTCCCCGATTCTGAACCAGTTGACTTATTTAGTGATGA	1546
Db	659	TTCTGAGCTAGTTGAAGATTCCCTCACCTGATTCTGAACCAGTTGACTTATTTAGTGATGA	718
Qy	1547	TTCAATACCCGAAGTTCCACAAAAACAAGATGAAGCTGTAATACTTGTGAAAGAAAACCT	1606
Db	719	TTCAATACCTGACGTTCCACAAAAACAAGATGAACTGTGATGCTTGTGAAAGAAAGTCT	778
Qy	1607	CAGTGAATTTTCATCTGAGTCAATGACAGGACATGACAATAAGGGAAAACCTCAGTGCTTC	1666
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Qy	1667	ACCATCACCTGAGGGAGGAAAACCGTATTTGGAGTCTTTTCAGCCAGTTTAGGCATCAC	1726
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Db	896	AAAAGATACCTGTTACCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAATTCCTTT	955
Qy	1787	GCAGATGGAGGAGCTCAATACTGCAGTTTATTCAAGTGATGGCTTATTCATTGCTCAGGA	1846
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Qy	1847	AGCAAAACCTAAGAGAAAGTGAACATTTTCAGATTTCATCTCCGATTGAGATTATAGATGA	1906
Db	1016	AGCACAGATAAGAGAAACTGAAACGTTTTTCAGATTTCATCTCCAATTGAAATTATAGATGA	1075
Qy	1907	GTTCCCGACCTTTGTCTAGTTCTAAAGCAGATTCTTCTCTACATTAGCCAGGGAATACAC	1966
Db	1076	GTTCCCTACATTGATCAGTTCTAAAACCTGATTCATTTTCTAAATTAGCCAGGGAATATAC	1135
Qy	1967	TGACCTAGAAAGTAGCCACAAAAGTGAAATTGCTGACATCCAGGATGGAGCTGGGTCATT	2026
Db	1136	TGACCTAGAAAGTATCCACAAAAGTGAAATTGCTAATGCCCCGGATGGAGCTGGGTCATT	1195
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Qy	2141	ACTGCCTCCAGATGTTTCTGCTTTGGATGCTCAAGCAGAGATAGGCAGCATAGAAAAACC	2200
Db	1316	ATTGCCTCCAGATGTTTCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACC	1375
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Qy	2321	CTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCTTGTTCCCTGCTGCTCTC	2380
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Qy	2381	GCTGACAGTATTCAGCATTGTGAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCTGT	2440
Db	1556	ATTGACAGTATTCAGCATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGT	1615
Qy	2441	GACTATCAGCTTTAGGATATATAAGGGTGTGATCCAGGCTATCCAGAAATCTGATGAAGG	2500
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Qy	2501	CCACCCATTACAGGGCATATTTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAA	2560
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Qy	2561	GTACAGCAATTCTGCTCTTGGTCATGTAACTGCACAATAAAAGAACTCAGACGCCTCTT	2620
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Db	1781	CTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTA	1840

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 Qy 2741 TGTTCCTGCTTGTTCATGGTCTGACACTACTGATTTTGGCTCTCATTTCCTTCAG 2800
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 Db 1901 TGTTCCTGCTTGTTCATGGTCTGACACTACTGATTTTGGCTCTCATTTCCTTCAG 1960
 Qy 2801 TAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAA 2860
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 Db 1961 TAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAA 2020
 Qy 2861 AGCTGAATGAGAAAGCCTGAAAGAGTTAACAATAGAGGAGTTTATCTTTAAAGGGGATAT 2920
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 Db 2021 AGCTGAATGAGAAAGCCTGAAAGAGTTAACAATAGAGGAGTTTATCTTTAAAGGGGATAT 2075
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 Db 2195 GTCTTGACTGCCCTGTGTTTCATCATCTTAAGTATTGTAAGCTGCTATGTATGGATTAA 2254
 Qy 3089 TCGTAATCATATTTGTTTTTCCTGTATGAGGCACTGGTGAATAAAACAAGATCTGAGAAA 3148
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 Db 2255 CCGTAATCATATTTGTTTTTCCTGTATGAGGCACTGGTGAATAAAACAAGATCTGAGAAA 2301
 Qy 3149 GCTGTATATTACACTTTGTGCGCAGGTAGTCTTGCTGTAT-TTGGGGAATTGCAAAGAAAG 3207
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 Db 2302 CCTGTATATTACTTTGTTGTCAGATAGTCTTGCCGCATCTTGCAAGTTGCAGAGATGG 2361
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 Db 2362 TGGAGCTAGAAAAAAA 2379

RESULT 15

AAF98399

ID AAF98399 standard; cDNA; 2386 BP.

XX

AC AAF98399;

XX

DT 07-JUN-2001 (first entry)

XX

DE Human cDNA clone BG160_1 sequence SEQ ID 41.

XX

KW Human; secreted protein; nutrient; cytokine modulator; proliferation;
 KW differentiation; immune system modulator; tissue growth; chemotactic;
 KW haemostatic; thrombolytic; anti-inflammatory; tumour inhibition; ss;
 KW haematopoiesis.

XX

OS Homo sapiens.

XX
 PN WO200119988-A1.
 XX
 PD 22-MAR-2001.
 XX
 PF 14-SEP-2000; 2000WO-US025135.
 XX
 PR 17-SEP-1999; 99US-00398829.
 XX
 PA (GEMY) GENETICS INST INC.
 XX
 PI Jacobs K, Mccoy JM, Lavallie ER, Collins-Racie LA, Evans C;
 PI Merberg D, Treacy M, Bowman MR, Spaulding V, Agostino MJ;
 XX
 DR WPI; 2001-244801/25.
 DR P-PSDB; AAB90682.
 XX
 PT Isolated nucleic acids encoding polypeptides, useful for modulating e.g.
 PT cytokine and cell proliferation/differentiation activity, the immune
 PT system and hematopoiesis regulating activity.
 XX
 PS Claim 1; Page 408-409; 557pp; English.
 XX
 CC Human cDNA clones represented in AAF98374 - AAF98489 encode secreted
 CC proteins AAB90667 - AAB90750. The cDNA clones are isolated from various
 CC tissue types, and may be used in the prevention, treatment and diagnosis
 CC of diseases associated with inappropriate protein expression. The
 CC polypeptides and nucleic acids may be used as nutrients or to modulate
 CC cytokine and cell proliferation/differentiation activity and may also be
 CC involved in modulation of the immune system. The cDNA sequences,
 CC proteins, their agonists and/or antagonists exhibit haematopoiesis
 CC regulating activity; tissue growth activity; activin/inhibin activity;
 CC chemotactic/chemokinetic activity; haemostatic and thrombolytic activity;
 CC receptor/ligand activity; anti-inflammatory activity; haematopoiesis
 CC activity; cadherin/tumour suppressor activity; and/or tumour inhibition
 CC activity. Included in the invention are probes represented in AAF98490 -
 CC AAF98572 which are specific for the cDNA clones encoding the secreted
 CC proteins
 XX
 SQ Sequence 2386 BP; 756 A; 448 C; 496 G; 686 T; 0 U; 0 Other;

Query Match 46.3%; Score 1774; DB 5; Length 2386;
 Best Local Similarity 86.8%; Pred. No. 0;
 Matches 2099; Conservative 0; Mismatches 260; Indels 59; Gaps 11;

Qy	827	CAAGACATCAAACCCTTTTCCTTATGGCAGCACAGGAGTCTAAGACAGATTACGTTACAAC	886
Db	2	CAAAACATCAAACCCTTTTCTTGTAGCAGCACAGGATTCTGAGACAGATTATGTCACAAC	61
Qy	887	AGATCATGTGTCAAAGGTGACCGAGGAAGTAGTGGCAAACATGCCTGAAGGTCTAACCCC	946
Db	62	AGATAATTTAACAAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCC	121
Qy	947	AGATTTGGTTCAGGAAGCATGTGAAAGTGAATTGAATGAAGCTACTGGTACAAAATTGC	1006
Db	122	AGATTTAGTACAGGAAGCATGTGAAAGTGAATTGAATGAAGTTACTGGTACAAAGATTGC	181

Qy	1007	CTTTGAAACAAAAATGGACCTGGTTCAAACCTTCAGAAGCTGTGCAGGAGTCACTTTACCC	1066
Db	182	TTATGAAACAAAAATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCC	241
Qy	1067	TGTAACACAGCTTTGCCCATCTTTTGAAGAATCTGAAGCTACTCCGTCACCGGTTTTGCC	1126
Db	242	TGCAGCACAGCTTTGCCCATCATTGAAGAGTCAGAAGCTACTCCTTCACCAGTTTTGCC	301
Qy	1127	TGACATTGTCATGGAAGCACCATTAAATTCTGTAGTTTCTAGTGCTGGTGCTTCTGCAGT	1186
Db	302	TGACATTGTTATGGAAGCACCATTGAATTCTGCAGTTTCTAGTGCTGGTGCTTCCGTGAT	361
Qy	1187	GCAGCTCAGTTCATCACCATTAGAACTCTTCCTTCAGTTAATTATGAAAGCATAAAGTT	1246
Db	362	ACAGCCCAGCTCATCACCATTAGAAGC---TTCTTCAGTTAATTATGAAAGCATAAAACA	418
Qy	1247	TGAGCCTGAAAATCCCCACCATATGAGGAGGCCATGAATGTATCACTAAAAAAGAATC	1306
Db	419	TGAGCCTGAAAACCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAGTATC	478
Qy	1307	AGGAATGAATGAAGAAATCACAGAGCCTGAAGGTATTAGTGTAGCTGTTTCAGGAAACAGA	1366
Db	479	AGGAATAAAGGAAGAAATTAAAGAGCCTGAAAATATTAATGCAGCTCTTCAAGAAACAGA	538
Qy	1367	AGCTCCTTATATATCTATTGCATGTGATTTAATTAAAGAAACAAAGATCTCTACTGAACC	1426
Db	539	AGCTCCTTATATATCTATTGCATGTGATTTAATTAAAGAAACAAAGCTTCTGCTGAACC	598
Qy	1427	GACTCCAGATTTCTCTAGTTATTTCAGAAATAGCAGAAGTTGCACAGCCAGTGCCCGAGCA	1486
Db	599	AGCTCCGATTTCTCTGATTATTTCAGAAATGGCAAAGTTGAACAGCCAGTGCCTGATCA	658
Qy	1487	TTCTGAGCTAGTTGAAGATTCCCTCCCCGATTCTGAACCAGTTGACTTATTTAGTGATGA	1546
Db	659	TTCTGAGCTAGTTGAAGATTCCCTCACCTGATTCTGAACCAGTTGACTTATTTAGTGATGA	718
Qy	1547	TTCAATACCCGAAGTTCCACAAAAACAAGATGAAGCTGTAATACTTGTGAAAGAAAACCT	1606
Db	719	TTCAATACCTGACGTTCCACAAAAACAAGATGAACTGTGATGCTTGTGAAAGAAAGTCT	778
Qy	1607	CACTGAAATTTTCATCTGAGTCAATGACAGGACATGACAATAAGGGAAAACCTCAGTGCTTC	1666
Db	779	CACTGAGACTTCATTTGAGTCAATGATAGAATATGAAAATAAGGAAAAACCTCAGTGCTTT	838
Qy	1667	ACCATCACCTGAGGGAGGAAAACCGTATTTGGAGTCTTTTCAGCCCAGTTTAGGCATCAC	1726
Db	839	GC---CACCTGAGGGAGGAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACAC	895
Qy	1727	AAAAGATACCTTAGCACCTGATGAAGTTTCAGCATTGACCCAAAAGGAGAAAATCCCTTT	1786
Db	896	AAAAGATACCCTGTTACCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAATTCCTTT	955
Qy	1787	GCAGATGGAGGAGCTCAATACTGCAGTTTATTCAAGTGATGGCTTATTCATTGCTCAGGA	1846
Db	956	GCAGATGGAGGAGCTCAGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGA	1015
Qy	1847	AGCAAACCTAAGAGAAAGTGAACATTTTCAGATTCATCTCCGATTGAGATTATAGATGA	1906

Db	1016	AGCACAGATAAGAGAAACTGAAACGTTTTTCAGATTTCATCTCCAATTGAAATTATAGATGA	1075
Qy	1907	GTTCCCGACCTTTGTCTAGTTCTAAAGCAGATTCTTCTCCTACATTAGCCAGGGAATACAC	1966
Db	1076	GTTCCCTACATTGATCAGTTCTAAAAGTATTCTTTCTAAATTAGCCAGGGAATATAC	1135
Qy	1967	TGACCTAGAAGTAGCCACAAAAGTGAAATTGCTGACATCCAGGATGGAGCTGGGTCATT	2026
Db	1136	TGACCTAGAAGTATCCACAAAAGTGAAATTGCTAATGCCCCGGATGGAGCTGGGTCATT	1195
Qy	2027	GGCTTGTGCAGGATTGCCCCATGACCTTTCTTTCAGAGTATACAACCTAAAGAGGAAGT	2086
Db	1196	GCCTTGCACAGAATTGCCCCATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGA	1255
Qy	2087	TCA-----TGTCCCAGATGAGTTCTCCAAAGATAGGGGTGATGTTTCAAAGGTGCCCGT	2140
Db	1256	GAAAATCAGTTTCTCAGATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTT	1315
Qy	2141	ACTGCCTCCAGATGTTTCTGCTTTGGATGCTCAAGCAGAGATAGGCAGCATAGAAAAACC	2200
Db	1316	ATTGCCTCCAGATGTTTCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACC	1375
Qy	2201	CAAAGTTCTTGTGAAAGAAGCCGAGAGAAAACCTTCCTTCTGATACAGAAAAAGAGCGAAG	2260
Db	1376	CAAAGTTCTTGTGAAAGAAGCTGAGAAAAAACTTCCTTCCGATACAGAAAAAGAGGACAG	1435
Qy	2261	ATCTCCATCTGCTATATTTTTCAGCAGAGCTGAGTAAACTTCAGTTGTTGACCTCCTCTA	2320
Db	1436	ATCACCATCTGCTATATTTTTCAGCAGAGCTGAGTAAACTTCAGTTGTTGACCTCCTGTA	1495
Qy	2321	CTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCTTGTTCCCTGCTGCTCTC	2380
Db	1496	CTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCCTATTCCTGCTGCTTTC	1555
Qy	2381	GCTGACAGTATTCAGCATTGTGAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCTGT	2440
Db	1556	ATTGACAGTATTCAGCATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGT	1615
Qy	2441	GACTATCAGCTTTAGGATATATAAGGGTGTGATCCAGGCTATCCAGAAATCTGATGAAGG	2500
Db	1616	GACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGG	1675
Qy	2501	CCACCCATTCAGGGCATATTTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAA	2560
Db	1676	CCACCCATTCAGG-----GAAGTTGCTATATCTGAGGAGTTGGTTCAGAA	1720
Qy	2561	GTACAGCAATTCTGCTCTTGGTCATGTTAAGTGCACAATAAAAGAACTCAGACGCCTCTT	2620
Db	1721	GTACAGTAATTCTGCTCTTGGTCATGTGAAGTGCACGATAAAGGAACTCAGGCGCCTCTT	1780
Qy	2621	CTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAAGTTGATGTGGGTATTTACCTA	2680
Db	1781	CTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAAGTTGATGTGGGTATTTACCTA	1840
Qy	2681	TGTTGGTGCCTTGTTCAATGGTCTGACACTACTAATTTTGGCTCTGATTTCACTCTTCAG	2740

Db	1841	TGTTGGTGCCTTGTTTAAATGGTCTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAG	1900
Qy	2741	TGTTCCCTGTTATTTATGAACGGCATCAGGCGCAAATAGATCATTATCTGGGACTTGCAAA	2800
Db	1901	TGTTGGTGTATTTATGAACGGCATCAGGCACAGATAGATCATTATCTAGGACTTGCAAA	1960
Qy	2801	TAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAA	2860
Db	1961	TAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAA	2020
Qy	2861	AGCTGAATGAGAAAGCCTGAAAGAGTTAACAATAGAGGAGTTTATCTTTAAAGGGGATAT	2920
Db	2021	AGCTGAATGAAAACGCCCAAATAATTA-----GTAGGAGTTCATCTTTAAAGGGGATAT	2075
Qy	2921	TCATTTGATTCCATTGGGGAGGGTCAGGGAAGAACAAAGCCTTGACATTGCAGTGCAGTT	2980
Db	2076	TCATTTGATTATACGGGGAGGGTCAGGGAAGAACGAA-CCTTGACGTTGCAGTGCAGTT	2134
Qy	2981	TCAC-----AGATCTTTATTTTGTAGCAACGCAGTG-TCTGAGGAAAAATGACCT	3028
Db	2135	TCACAGATCGTTGTTAGATCTTTATTTTGTAGCCATGCACTGTTGTGAGGAAAAATTACCT	2194
Qy	3029	GTCTTGACTGCCCTGTGTTTCATCATCTTAAGTATTGTAAGCTGCTATGTATGGATTTAAA	3088
Db	2195	GTCTTGACTGCCATGTGTTTCATCATCTTAAGTATTGTAAGCTGCTATGTATGGATTTAAA	2254
Qy	3089	TCGTAATCATATTTGTTTTTCCTGTATGAGGCACTGGTGAATAAACAAAGATCTGAGAAA	3148
Db	2255	CCGTAATCATA--TCTTTTTCCTATCTGAGGCACTGGTGGA-----ATAAAAAA	2301
Qy	3149	GCTGTATATTACACTTTGTGCGAGGTAGTCTTGCTGTAT-TTGGGGAATTGCAAAGAAAAG	3207
Db	2302	CCTGTATATTTTACTTTGTTGCAGATAGTCTTGCCGCATCTTGCCAAGTTGCAGAGATGG	2361
Qy	3208	TGGAGCTGACAGAAATAA	3225
Db	2362	TGGAGCTAGAAAAAAA	2379

Search completed: September 11, 2004, 02:15:15
Job time : 1353.11 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 11, 2004, 01:30:35 ; Search time 237.854 Seconds
(without alignments)
8942.975 Million cell updates/sec

Title: US-09-830-972-28
Perfect score: 3833
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Scoring table: IDENTITY_NUC
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Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query		DB	ID	Description
	Score	Match Length			
1	2687.8	70.1 4822	4	US-09-484-970B-106	Sequence 106, App
2	789.8	20.6 2610	4	US-09-023-655-382	Sequence 382, App
3	590.8	15.4 799	2	US-08-700-607-2	Sequence 2, Appli
4	293.4	7.7 536	4	US-09-621-976-3839	Sequence 3839, Ap
5	254.4	6.6 508	4	US-09-621-976-3840	Sequence 3840, Ap
6	230.4	6.0 1766	4	US-09-149-476-254	Sequence 254, App
7	230.4	6.0 2664	4	US-09-149-476-255	Sequence 255, App
8	202.2	5.3 1095	2	US-08-700-607-4	Sequence 4, Appli
9	182	4.7 794	4	US-09-149-476-102	Sequence 102, App
10	174.2	4.5 261	2	US-08-700-607-9	Sequence 9, Appli
11	138.6	3.6 301	4	US-09-439-313-279	Sequence 279, App

12	138.6	3.6	301	4	US-09-352-616A-279	Sequence 279, App
13	138.6	3.6	301	4	US-09-232-149A-279	Sequence 279, App
14	138.6	3.6	301	4	US-09-159-812-279	Sequence 279, App
15	138.6	3.6	301	4	US-09-636-215-279	Sequence 279, App
16	138.6	3.6	301	4	US-09-685-166A-279	Sequence 279, App
17	138.6	3.6	301	4	US-09-688-489-279	Sequence 279, App
18	113.6	3.0	211	4	US-09-506-729-51	Sequence 51, Appl
c 19	69.4	1.8	7218	1	US-08-232-463-14	Sequence 14, Appl
20	60.8	1.6	200	3	US-09-221-298-100	Sequence 100, App
21	60.8	1.6	200	4	US-09-401-064-100	Sequence 100, App
22	46.6	1.2	3095	6	5231168-1	Patent No. 5231168
c 23	45	1.2	832	4	US-09-621-976-2813	Sequence 2813, Ap
24	44	1.1	1134	3	US-09-248-335-29	Sequence 29, Appl
c 25	43.8	1.1	1949	4	US-08-961-527-289	Sequence 289, App
26	43.6	1.1	2439	3	US-09-386-493-1	Sequence 1, Appli
c 27	42.8	1.1	949	3	US-08-714-918-12	Sequence 12, Appl
c 28	42.8	1.1	949	3	US-09-265-315-12	Sequence 12, Appl
c 29	42.8	1.1	949	3	US-09-265-315-12	Sequence 12, Appl
c 30	42.8	1.1	949	3	US-09-266-417-12	Sequence 12, Appl
c 31	42.8	1.1	949	4	US-09-528-709-12	Sequence 12, Appl
c 32	42.8	1.1	949	4	US-09-527-745-12	Sequence 12, Appl
c 33	42.8	1.1	1739	3	US-08-714-918-1	Sequence 1, Appli
c 34	42.8	1.1	1739	3	US-09-265-315-1	Sequence 1, Appli
c 35	42.8	1.1	1739	3	US-09-265-315-1	Sequence 1, Appli
c 36	42.8	1.1	1739	3	US-09-266-417-1	Sequence 1, Appli
c 37	42.8	1.1	1739	4	US-09-528-709-1	Sequence 1, Appli
c 38	42.8	1.1	1739	4	US-09-527-745-1	Sequence 1, Appli
39	42.8	1.1	3124	4	US-09-112-580-8	Sequence 8, Appli
c 40	42.8	1.1	6645	4	US-08-956-171E-259	Sequence 259, App
41	42.4	1.1	2671	6	5168051-9	Patent No. 5168051
42	42	1.1	277	3	US-09-007-005-3	Sequence 3, Appli
43	42	1.1	277	3	US-09-244-796-3	Sequence 3, Appli
44	41.6	1.1	21234	4	US-09-810-671-3	Sequence 3, Appli
45	41.6	1.1	21234	4	US-10-109-854-3	Sequence 3, Appli

ALIGNMENTS

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RESULT 1
US-09-484-970B-106
; Sequence 106, Application US/09484970B
; Patent No. 6426186
; GENERAL INFORMATION:
; APPLICANT: Jones, Karen A.
; APPLICANT: Volkmuth, Wayne
; APPLICANT: Walker, Michael G.
; TITLE OF INVENTION: BONE REMODELING GENES
; FILE REFERENCE: PB-0014 US
; CURRENT APPLICATION NUMBER: US/09/484,970B
; CURRENT FILING DATE: 2000-01-18
; NUMBER OF SEQ ID NOS: 172
; SOFTWARE: PERL Program
; SEQ ID NO 106
; LENGTH: 4822
; TYPE: DNA
; ORGANISM: Homo sapiens

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; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6426186 444857.15CB1
; NAME/KEY: unsure
; LOCATION: 33, 51, 79, 211, 369, 483-484, 731, 748, 4803, 4805-4806, 4808-4809,
; OTHER INFORMATION: a, t, c, g, or other
US-09-484-970B-106

Query Match 70.1%; Score 2687.8; DB 4; Length 4822;
Best Local Similarity 85.6%; Pred. No. 0;
Matches 3333; Conservative 0; Mismatches 458; Indels 104; Gaps 27;

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Qy      1 CTATCTCCTCTCTCAGCCGCTGCTTTTAAAGAACGTGAATACCTTGGTGATTTACCAGCA 60
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Qy      61 GTACTGCCCCACTGAAGGAACACTTCCAGCAACTTCAAATGAAGCTTCTAAAGCATTCTCA 120
      ||| | |||||
Db     1024 GTATTACCCACTGAAGGAACACTTCAAGAAAATGTCAGTGAAGCTTCTAAAGAGGTCTCA 1083

Qy     121 GAGAAGGCCAAAAATCCATTTGTAGAGAGAAATTTAACAGAATTTTCAGAATTGGAATAT 180
      |||||
Db     1084 GAGAAGGCCAAAACTCTACTCATAGATAGAGATTTAACAGAGTTTTCAGAATTAGAATAC 1143

Qy     181 TCAGAAATGGAATCATCATTTCAGTGGCTCTCAAAAGGCAGAACCTGCCGTAACAGTAGCG 240
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Db     1144 TCAGAAATGGGATCATCGTTTCAGTGTCTCTCCAAAAGCAGAATCTGCCGTAATAGTAGCA 1203

Qy     241 AATCCTAGGGACGAAATAGTTGTGAGGAGTAGAGATAAAGAAGAGGACTTAGTTAGTCTT 300
      |||||
Db     1204 AATCCTAGGGAAGAAATAATCGTGAAAAATAAAGATGAAGAAGAGAAGTTAGTTAGTAAT 1263

Qy     301 AACATCCTTCATACTCAGCAGGAGTTATCTACAGTCCTTACGAAATCAGTTGAAGAAGAA 360
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Db     1264 AACATCCTTCATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGGTTAAAGAGGAT 1323

Qy     361 GATAGAGTTCTGTCTCCAGAAAAAACAAAGGACAGTTTTTAAGGAAAAGGGAGTTGCAGCA 420
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Db     1324 GA---AGTTGTGTCTTCAGAAAAAGCAAAGACAGTTTTTAATGAAAAGAGAGTTGCAGTG 1380

Qy     421 GAAGCTTCTATGGGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTG 480
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Db     1381 GAAGCTCCTATGAGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTG 1440

Qy     481 AAAGATACTTACAAGCAAGATAGTGATGTTTTGATTGCTGGAGGTAATATAGAGAGCAAA 540
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Qy     541 TTGGAAGGTAAAGTGGATAAGAAACACTTTTCAGATAGCCTTGAACAAACAAATCGTGAA 600
      |||||
Db     1498 TTGGAAAGTAAAGTGGATAAAAAATGTTTTGCAGATAGCCTTGAGCAAACATAATCACGAA 1557

Qy     601 AAAGATAGTGAAAGCAGTAATGATGACACTTCATTTCCCAGTACACCAGAAGCTGTAAGA 660
      |||||
Db     1558 AAAGATAGTGAGAGTAGTAATGATGATACTTCTTTCCCCAGTACGCCAGAAGGTATAAAG 1617
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Qy 661 GGTGGTTCGGGAGCGTACATCACGTGTGCTCCCTTTAACC---CAACAACTGAGAATGTT 717
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Qy 718 TCAACAAACATTTTTCCCTTGTTGGAAGATCATACTTCGGAAAATAAGACAGATGAAAAA 777
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 Db 1678 GCAACAAACATTTTTCCCTTGTTAGGAGATCCTACTTCAGAAAATAAGACCGATGAAAAA 1737

Qy 778 AAGA--TAGAAAAAAAAAAGGCACAAATTGTAACAGAGAAGAATGCAAGTGTCAAGACATC 835
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 Db 1738 AAAAATAGAAGAAAAGAAGGCCCAAATAGTAACAGAGAAGAATACTAGCACCAAAACATC 1797

Qy 836 AAACCC-TTTCCTTATGGCAGCACAGGAGTCTAAGACAGATTACGTTACAACAGATCATG 894
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 Db 1798 AAACCTTTTACTTGTTAGCAGCACAGGATTCTGAGACAGATTATGTCACAACAGATAATT 1857

Qy 895 TGTCAAAGGTGACCGAGGAAGTAGTGGCAAACATGCCTGAAGGTCTAACCCAGATTGG 954
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 Db 1858 TAACAAAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCCAGATTAG 1917

Qy 955 TTCAGGAAGCATGTGAAAGTGAATTGAATGAAGCTACTGGTACAAAAATTGCCTTTGAAA 1014
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 Db 1918 TACAGGAAGCATGTGAAAGTGAATTGAATGAAGTACTGGTACAAAGATTGCTTATGAAA 1977

Qy 1015 CAAAAATGGACCTGGTTCAAACCTCAGAAGCTGTGCAGGAGTCACTTTACCCTGTAACAC 1074
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 Db 1978 CAAAAATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCAC 2037

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 Db 2038 AGCTTTGCCCATCATTTGAAGAGTCAGAAGCTACTCCTTCACCAGTTTTGCCTGACATTG 2097

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 Db 2098 TTATGGAAGCACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGATACAGCCCA 2157

Qy 1195 GTTCATCACCATTAGAACTCTTCCTTCAGTTAATTATGAAAGCATAAAGTTTGAGCCTG 1254
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 Db 2158 GTCATCACCATTAGAAGC---TTCTTCAGTTAATTATGAAAGCATAAAACATGAGCCTG 2214

Qy 1255 AAAATCCCCCACCATATGAGGAGGCCATGAATGTATCACTAAAAAAGAATCAGGAATGA 1314
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 Db 2215 AAAACCCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAGTATCAGGAATAA 2274

Qy 1315 ATGAAGAAATCACAGAGCCTGAAGGTATTAGTGTAGCTGTTCAGGAAACAGAAGCTCCTT 1374
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 Db 2275 AGGAAGAAATTAAAGAGCCTGAAAATATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTT 2334

Qy 1375 ATATATCTATTGCATGTGATTTAATTAAAGAAACAAAGATCTCTACTGAACCGACTCCAG 1434
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 Db 2335 ATATATCTATTGCATGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAACCGACTCCGG 2394

Qy 1435 ATTTCTCTAGTTATTCAGAAATAGCAGAAGTTGCACAGCCAGTGCCCGAGCATTCTGAGC 1494
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 Db 2395 ATTTCTCTGATTATTCAGAAATGGCAAAAGTTGAACAGCCAGTGCCTGATCATTCTGAGC 2454

Qy 1495 TAGTTGAAGATTCCTCCCCGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATAC 1554

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QY	1555	CCGAAGTTCCACAAAAACAAGATGAAGCTGTAATACTTGTGAAAGAAAACCTCACTGAAA	1614
Db	2515	CTGACGTTCCACAAAAACAAGATGAAACTGTGATGCTTGTGAAAGAAAGTCTCACTGAGA	2574
QY	1615	TTTCATCTGAGTCAATGACAGGACATGACAATAAGGGAAAACCTCAGTGCTTCACCATCAC	1674
Db	2575	CTTCATTTGAGTCAATGATAGAATATGAAAATAAGGAAAAACCTCAGTGCTTTGC---CAC	2631
QY	1675	CTGAGGGAGGAAAACCGTATTTGGAGTCTTTTCAGCCCAGTTTAGGCATCACAAAAGATA	1734
Db	2632	CTGAGGGAGGAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATA	2691
QY	1735	CCTTAGCACCTGATGAAGTTTCAGCATTGACCCAAAAGGAGAAAAATCCCTTTGCAGATGG	1794
Db	2692	CCCTGTTACCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAAATTCCTTTGCAGATGG	2751
QY	1795	AGGAGCTCAATACTGCAGTTTATTCAAGTGATGGCTTATTCATTGCTCAGGAAGCAAACC	1854
Db	2752	AGGAGCTCAGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGA	2811
QY	1855	TAAGAGAAAGTGAAACATTTTCAGATTTCATCTCCGATTGAGATTATAGATGAGTTCCCGA	1914
Db	2812	TAAGAGAAACTGAAACGTTTTCAGATTTCATCTCCAATTGAAATTATAGATGAGTTCCCTA	2871
QY	1915	CCTTTGTGCTAGTTCTAAAGCAGATTCTTCTCCTACATTAGCCAGGGAATACACTGACCTAG	1974
Db	2872	CATTGATCAGTTCTAAAACTGATTCAATTTCTAAATTAGCCAGGGAATATACTGACCTAG	2931
QY	1975	AAGTAGCCCAACAAAAGTGAAATTGCTGACATCCAGGATGGAGCTGGGTTCATTGGCTTGCTG	2034
Db	2932	AAGTATCCCAACAAAAGTGAAATTGCTAATGCCCGGATGGAGCTGGGTTCATTGCCTTGCA	2991
QY	2035	CAGGATTGCCCCATGACCTTTCTTTCAAGAGTATACAACC-----TAAAGAGGAAGTTC	2088
Db	2992	CAGAATTGCCCCATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCA	3051
QY	2089	ATGTCCCAGATGAGTTCTCCAAAGATAGGGGTGATGTTTCAAAGGTGCCCGTACTGCCTC	2148
Db	3052	GTTTCTCAGATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTC	3111
QY	2149	CAGATGTTTCTGCTTTGGATGCTCAAGCAGAGATAGGCAGCATAGAAAAACCCAAAGTTC	2208
Db	3112	CAGATGTTTCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTC	3171
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Db	3172	TTGTGAAAGAAGCTGAGAAAAACCTCCTTCCGATACAGAAAAAGAGGACAGATCACCAT	3231
QY	2269	CTGCTATATTTTTCAGCAGAGCTGAG-TAAAACTTCAGTTGTTGACCTCCTCTACTGGAGA	2327
Db	3232	CTGCTATATTTTTCAGCAGAGCTGAGCTAAAACTTCAGTTGTTGACCTCCTGTACTGGAGA	3291
QY	2328	GACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCTTGTTTCCTGCTGCTCTCGCTGACA	2387

Db	3292	GACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCCTATTCCTGCTGCTTTCATTGACA	3351
QY	2388	GTATTCAGCATTGTGAGTGTAAACGGCCTACATTGCCTTGGCCCTGCTCTCTGTGACTATC	2447
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QY	2448	AGCTTTAGGATATATAAGGGTGTGATCCAGGCTATCCAGAAATCTGATGAAGGCCACCCA	2507
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QY	2508	TTCAGGGCATATTTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGC	2567
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Db	3592	GATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGT	3651
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Db	3652	GCCTTGTTTAAATGGTCTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTTCCCT	3711
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Db	3712	GTTATTTATGAACGGCATCAGGCACAGATAGATCATTATCTAGGACTTGCAAATAAGAAT	3771
QY	2808	GTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGAA	2867
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QY	2868	TGAGAAAGCCTGAAAGAGTTAACAATAGAGGAGTTTATCTTTAAAGGGGATATTCATTTG	2927
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Db	4006	CTGCCATGTGTTTCATCATCTTAAGTATTGTAAGCTGCTATGTATGGATTTAAACCGTAAT	4065
QY	3096	CATATTTGTTTTTCTGTATGAGGCACCTGGTGAATAAACAAAGATCTGAGAAAGCTGTAT	3155
Db	4066	CATA--TCTTTTTCTATCTGAGGCACCTGGTGA-----ATAAAAAACCTGTAT	4112
QY	3156	ATTACACTTTGTGCGAGGTAGTCTTGCTGTAT-TTGGGGAATTGCAAAGAAAGTGGAGCT	3214
Db	4113	ATTTTACTTTGTTGCAGATAGTCTTGCCGCATCTTGGCAAGTTGCAGAGATGGTGGAGCT	4172


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Qy      3215 -----GACAGAAATAACCCTTTTCACAGTTTGTGCACTGTGTACGGTCTGTGTAGGT 3266
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Db      4173 AGAAAAAAAAAAAAAAAAAGCCCTTTTCAGTTTGTGCACTGTGTATGGTCCGTGTAGAT 4232

Qy      3267 TGATGCAGATTTTCTGAAATGAAA-----TGTTTAGACGAGATCATGCCACCAAGGCAGGA 3322
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Db      4233 TGATGCAGATTTTCTGAAATGAAATGTTTGTTTAGACGAGATCATACCGGTAAAGCAGGA 4292

Qy      3323 GTGAAAAGCTTGCCTTTCTGGTATGTTCTAGGTGTATTGTGAAATTTACTGTTGTATT 3382
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Db      4293 ATGACAAAGCTTG-CTTTTCTGGTATGTTCTAGGTGTATTGTGACTTTTACTGTTATATT 4351

Qy      3383 AATTGCCAATATAAGTAAATATAGATTATATATATCTATATATAGTGTTTCACGAAGCTT 3442
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Db      4352 AATTGCCAATATAAGTAAATATAGATTATATATG-----TATAGTGTTTCACAAAGCTT 4405

Qy      3443 AGCCCTTTACCTTCCCAGCTGCCCCACAGTGCTTGATACT-----TCTGTCTATGGGTTT 3496
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Db      4406 AGACCTTTACCTT-CCAGCCACCCACAGTGCTTGATAATTCAGAGTCAGTCATTGGTTA 4464

Qy      3497 TATGTGTGTAGTCCCAAAGCACATAAGCTAGGGAGAAACGTACTTCTAGGCGCACTACCA 3556
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Db      4465 TACATGTGTAGTTCCCAAAGCACATAAGCTAGAAGAAGAAATATTTCTAGGAGCACTACCA 4524

Qy      3557 TCTGTTTTCAACACGAACCGACGCCATGCAAACAGAACTCC-TCAACATAAACTTCACTG 3615
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      4525 TCTGTTTTCAACATGAA--ATGCCACACACATAGAACTCCAACAACATCAATTTTCATTG 4581

Qy      3616 CACAGACTTACTGTAGTTAATTTTATCAC--AAACTCTGGACTGAATCTAATGCTTCCAA 3673
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Db      4582 CACAGACTGACTGTAGTTAATTTTGTACAGAATCTATGGACTGAATCTAATGCTTCCAA 4641

Qy      3674 AAA-----TGTTTGCAAATATCAAACATTGTTATGTAAGAAAATAT-----AAAT 3718
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      4642 AAATGTTGTTTGTGTTTGCAAATATCAAACATTGTTATGCAAGAAATTATTAATTACAAAAT 4701

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Db      4702 GAAGATTTATACCATTGTGGTTTAAAGCTGTACTGAACTAAATCTGTGGAATGCATTGTGA 4761

Qy      3779 ACTGTAAAAGCAAAGTATCAATAAAGCTTATAGACTTAAAAAAAAAAAAAAAAAAAA 3833
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      4762 ACTGTAAAAGCAAAGTATCAATAAAGCTTATAGACTTAAAANGNNANNAGNGAAA 4816

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RESULT 2

US-09-023-655-382

; Sequence 382, Application US/09023655

; Patent No. 6607879

; GENERAL INFORMATION:

; APPLICANT: Cocks, Benjamin G.

; APPLICANT: Susan G. Stuart

; APPLICANT: Jeffrey J. Seilhamer

; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE

; TITLE OF INVENTION: EXPRESSION

; NUMBER OF SEQUENCES: 1508

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; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 382:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2610 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: LUNGNOT14
; CLONE: 1508778
US-09-023-655-382

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Query Match          20.6%; Score 789.8; DB 4; Length 2610;
Best Local Similarity 84.5%; Pred. No. 5.2e-190;
Matches 1021; Conservative 0; Mismatches 138; Indels 49; Gaps 10;

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Qy      2304 GTTGTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGC 2363
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Db      1311 GTTGTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGC 1370
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Qy      2364 TTGTTCTGCTGCTCTCGCTGACAGTATTCAGCATTGTGAGTGTAACGGCCTAC-ATTGC 2422
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Db      1371 CTATTCCTGCTGCTTTTCATTGACAGTATTCAGCATTGTGAGCGTAACAGCCTACAATTGC 1430
          |||

Qy      2423 CTTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAAGGGTGTGATCCAGGCTAT 2482
          |||
Db      1431 CTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTAT 1490
          |||

Qy      2483 CCAGAAATCTGATGAAGGCCACCCATTCAGGGCATATTTGGAATCTGAAGTTGCTATATC 2542
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Db      1491 CCAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGAAGTTGCTATATC 1550
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Qy	2543	TGAGGAGTTGGTTCAGAAGTACAGCAATTCTGCTCTTGGTCATGTAACTGCACAATAAAA	2602
Db	1551	TGAGGAGTTGGTTCAGAAGTACAGTAATTCTGCTCTTGGTCATGTGAAGTGCACGATAAAA	1610
Qy	2603	AGAACTCAGACGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTT	2662
Db	1611	GGAATCAGGCGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTT	1670
Qy	2663	GATGTGGGTATTTACCTATGTTGGTGCCTTGTTCAATGGTCTGACACTACTAATTTTGGC	2722
Db	1671	GATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAAATGGTCTGACACTACTGATTTTGGC	1730
Qy	2723	TCTGATTTCACTCTTCAGTGTTCCCTGTTATTTATGAACGGCATCAGGCGCAAATAGATCA	2782
Db	1731	TCTCATTTCACTCTTCAGTGTTCCCTGTTATTTATGAACGGCATCAGGCACAGATAGATCA	1790
Qy	2783	TTATCTGGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAAT	2842
Db	1791	TTATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAAT	1850
Qy	2843	CCCTGGATTGAAGCGTAAAGCTGAATGAGAAAAGCCTGAAAGAGTTAACAATAGAGGAGTT	2902
Db	1851	CCCTGGGTTGAAGCGCAAAGCTGAATGAAAACGCCCAAATAATTA-----GTAGGAGTT	1905
Qy	2903	TATCTTTAAAGGGGATATTCATTTGATTCCATTGGGGAGGGTCAGGGAAGAACAAAGCCT	2962
Db	1906	CATCTTTAAAGGGGATATTCATTTGATTTATACGGGGAGGGTCAGGGAAGAACGAACCT	1965
Qy	2963	TGACATTGCAGTGCAGTTTCAC-----AGATCTTTATTTTATAGCAACGCAGTG-	3010
Db	1966	TGACGTTGCAGTGCAGTTTCACAGATCGTTGTTAGATCTTTATTTTATGCCATGCACTGT	2025
Qy	3011	TCTGAGGAAAAATGACCTGTCTTGACTGCCCTGTGTTTCATCATCTTAAGTATTGTAAGCT	3070
Db	2026	TGTGAGGAAAAATTACCTGTCTTGACTGCCATGTGTTTCATCATCTTAAGTATTGTAAGCT	2085
Qy	3071	GCTATGTATGGATTTAAATCGTAATCATATTTGTTT--TTCCTGTATGAGGCACTGGTGA	3128
Db	2086	GCTATGTATGGATTTAAACCGTAATCATATCTTTTTCTATCTATCTGAGGCACTGGTGG	2145
Qy	3129	ATAAACAAAGATCTGAGAAAGCTGTATATTACACTTTGTGCGAGGTAGTCTTGCTGTAT-	3187
Db	2146	A-----ATAAAAAACCTGTATATTTTACTTTGTTGCAGATAGTCTTGCCGCATC	2194
Qy	3188	TTGGGGAATTGCAAAGAAAGTGGAGCT-----GACAGAAATAACCCCTTTTCACAGTTT	3240
Db	2195	TTGGCAAGTTGCAGAGATGGTGGAGCTAGAAAAANAAAGAAAAAGAGCCCTTTTCAGTTT	2254
Qy	3241	GTGCACTGTGTACGGTCTGTGTAGGTTGATGCAGATTTTCTGAAATGAAA---TGTTTA	3296
Db	2255	GTGCACTGTGTATGGTCCGTGTAGATTGATGCAGATTTTCTGAAATGAAATGTTTGTTTA	2314
Qy	3297	GACGAGATCATGCCACCAAGGCAGGAGTGAAAAAGCTTGCCTTTCTGGTATGTTCTAGG	3356
Db	2315	GACGAGATCATACCCGGTAAAGCAGGAATGACAAAGCTTGCTTTTCTGGTATGTTCTAGG	2374

Query Match 15.4%; Score 590.8; DB 2; Length 799;
 Best Local Similarity 92.9%; Pred. No. 7e-140;
 Matches 643; Conservative 0; Mismatches 42; Indels 7; Gaps 2;

Qy	2304	GTTGTTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGC	2363
Db	108	GTTGTTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGC	167
Qy	2364	TTGTTCCCTGCTGCTCTCGCTGACAGTATTCAGCATTGTGAGTGTAAACGGCCTACATTGCC	2423
Db	168	CTATTCCTGCTGCTTTCATTGACAGTATTCAGCATTGTGAGCGTAACAGCCTACATTGCC	227
Qy	2424	TTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAAGGGTGTGATCCAGGCTATC	2483
Db	228	TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC	287
Qy	2484	CAGAAATCTGATGAAGGCCACCCATTCAGGGCATATTTGGAATCTGAAGTTGCTATATCT	2543
Db	288	CAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGAAGTTGCTATATCT	347
Qy	2544	GAGGAGTTGGTTCAGAAGTACAGCAATTCTGCTCTTGGTCATGTAACTGCACAATAAAA	2603
Db	348	GAGGAGTTGGTTCAGAAGTACAGTAATTCTGCTCTTGGTCATGTGAAGTGCACGATAAAG	407
Qy	2604	GAACTCAGACGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTG	2663
Db	408	GAACTCAGGCGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTG	467
Qy	2664	ATGTGGGTATTTACCTATGTTGGTGCCTTGTTCAATGGTCTGACACTACTAATTTTGGCT	2723
Db	468	ATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAAATGGTCTGACACTACTGATTTTGGCT	527
Qy	2724	CTGATTTCACTCTTCAGTGTTCTGTTATTTATGAACGGCATCAGGCGCAAATAGATCAT	2783
Db	528	CTCATTTCACTCTTCAGTGTTCTGTTATTTATGAACGGCATCAGGCACAGATAGATCAT	587
Qy	2784	TATCTGGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATC	2843
Db	588	TATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATC	647
Qy	2844	CCTGGATTGAAGCGTAAAGCTGAATGAGAAAGCCTGAAAGAGTTAACAATAGAGGAGTTT	2903
Db	648	CCTGGATTGAAGCGCAAAGCTGAATGAAAACGCCCAAATAATTA-----GTAGGAGTTC	702
Qy	2904	ATCTTTAAAGGGGATATTCATTTGATTCCATTGGGGAGGGTCAGGGAAGAACAAGCCTT	2963
Db	703	ATCTTTAAAGGGGATATTCATTTGATTATACGGGGAGGGTCAGGGAAGAACGA--CCTT	760
Qy	2964	GACATTGCAGTGCAGTTTCACAGATCTTTATT	2995
Db	761	GACGTTGCAGTGCAGTTTCACAGATCGTTGTT	792

RESULT 4

US-09-621-976-3839

; Sequence 3839, Application US/09621976

; Patent No. 6639063
 ; GENERAL INFORMATION:
 ; APPLICANT: Dumas Milne Edwards, J.B.
 ; APPLICANT: Jobert, S.
 ; APPLICANT: Giordano, J.Y.
 ; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
 ; FILE REFERENCE: GENSET.054PR2
 ; CURRENT APPLICATION NUMBER: US/09/621,976
 ; CURRENT FILING DATE: 2000-07-21
 ; NUMBER OF SEQ ID NOS: 19335
 ; SOFTWARE: Patent.pm
 ; SEQ ID NO 3839
 ; LENGTH: 536
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 3..224
 US-09-621-976-3839

Query Match 7.7%; Score 293.4; DB 4; Length 536;
 Best Local Similarity 82.8%; Pred. No. 1.1e-64;
 Matches 443; Conservative 0; Mismatches 56; Indels 36; Gaps 8;

Qy	3291	TGTTTAGACGAGATCATGCCACCAAGGCAGGAGTGAAAAAGCTTGCCTTTCCTGGTATGT	3350
Db	13	TGTTTAGACGAGATCATACCGGTAAAGCAGGAATGACAAAGCTTGCTTTT-CTGGTATGT	71
Qy	3351	TCTAGGTGTATTGTGAAATTTACTGTTGTATTAATTGCCAATATAAGTAAATATAGATTA	3410
Db	72	TCTAGGTGTATTGTGACTTTTACTGTTATATTAATTGCCAATATAAGTAAATATAGATTA	131
Qy	3411	TATATATCTATATATAGTGTTCACGAAGCTTAGCCCTTTACCTTCCCAGCTGCCCCACA	3470
Db	132	TA-----TATGTATAGTGTTCACAAAGCTTAGACCTTTACCTT-CCAGCCACCCCACA	184
Qy	3471	GTGCTTGATACT-----TCTGTCATGGGTTTTATGTGTGTAGTCCCAAAGCACATAAGC	3524
Db	185	GTGCTTGATATTTTCAGAGTCAGTCATTGGTTATACATGTGTAGTTCCCAAAGCACATAAGC	244
Qy	3525	TAGGGAGAAACGTACTTCTAGGCGCACTACCATCTGTTTTCAACACGAACCGACGCCATG	3584
Db	245	TAGAAGAAGAAATATTTCTAGGAGCACTACCATCTGTTTTCAACATGAAATGCC-----A	299
Qy	3585	CAACAGAACTCCTCAACATAAACTTCACTGCACAGACTTACTGTAGTTAATTTTATCAC	3644
Db	300	CACACATAGAACTCCAACATCAATTTTCATTGCACAGACTGACTGTAGTTAATTTTGTAC	359
Qy	3645	--AAACTCTGGACTGAATCTAATGCTTCCAAAAATGTT-----TGCAAATATCAAACA	3695
Db	360	AGAATCTATGGACTGAATCTAATGCTTCCAAAAATGTTGTTTGTGTTTGCAAATATCAAACA	419
Qy	3696	TTGTTATGTAAGAAAATAT-----AAATGACGATTATACAATTGTGGTTTAAGCTG	3747
Db	420	TTGTTATGCAAGAAATTATTAATTACAAAATGAAGATTATACCATTGTGGTTTAAGCTG	479
Qy	3748	TATTGAACTAAATCTGTGGAATGCATTGTGAACTGTAAAAGCAAAGTATCAATAA	3802

Db 360 AGAATCTATGGACTGAATCTAATGCTTCCAAAAATGTTGTTTGTGTTGCAAATATCAAACA 419

QY 3696 TTGTTATGTAAGAAAATAT-----AAATGACGATTATACAATTGTGGTTTAAGCTG 3747
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Db 420 TTGTTATGCAAGAAATTATTAATTACAAAATGAAGATTATACCATTGTGGTTTAAGCTG 479

QY 3748 TATTGAACTAAATCTG 3763
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Db 480 TACTGAACTAAATCTG 495

RESULT 6

US-09-149-476-254

; Sequence 254, Application US/09149476
 ; Patent No. 6420526
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: 186 Human Secreted proteins
 ; FILE REFERENCE: PZ002P1
 ; CURRENT APPLICATION NUMBER: US/09/149,476
 ; CURRENT FILING DATE: 1998-09-08
 ; EARLIER APPLICATION NUMBER: PCT/US98/04493
 ; EARLIER FILING DATE: 1998-03-06
 ; EARLIER APPLICATION NUMBER: 60/040,162
 ; EARLIER FILING DATE: 1997-03-07
 ; EARLIER APPLICATION NUMBER: 60/040,333
 ; EARLIER FILING DATE: 1997-03-07
 ; EARLIER APPLICATION NUMBER: 60/038,621
 ; EARLIER FILING DATE: 1997-03-07
 ; EARLIER APPLICATION NUMBER: 60/040,626
 ; EARLIER FILING DATE: 1997-03-07
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 ; EARLIER FILING DATE: 1997-03-07
 ; EARLIER APPLICATION NUMBER: 60/040,336
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 ; EARLIER APPLICATION NUMBER: 60/047,615
 ; EARLIER FILING DATE: 1997-05-23
 ; EARLIER APPLICATION NUMBER: 60/047,597
 ; EARLIER FILING DATE: 1997-05-23
 ; EARLIER APPLICATION NUMBER: 60/047,502
 ; EARLIER FILING DATE: 1997-05-23
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 ; EARLIER APPLICATION NUMBER: 60/047,592
 ; EARLIER FILING DATE: 1997-05-23

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; EARLIER FILING DATE: 1997-04-11
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; EARLIER FILING DATE: 1997-06-06
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; EARLIER APPLICATION NUMBER: 60/047,589
; EARLIER FILING DATE: 1997-05-23

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; EARLIER APPLICATION NUMBER: 60/057,650
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; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,669
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02

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Query Match          6.0%; Score 230.4; DB 4; Length 1766;
Best Local Similarity 63.6%; Pred. No. 1.8e-48;
Matches 351; Conservative 0; Mismatches 201; Indels 0; Gaps 0;

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Qy      2300 TTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGC 2359
          | | | |      | | | | | | | | | | | | | | | | | | | | | | |
Db      286  TGCGGTGCACGATCTGATTTTCTGGAGAGATGTGAAGAAGACTGGGTTTGTCTTTGGCAC 345

Qy      2360 CAGCTTGTTCTGCTGCTCTCGCTGACAGTATTCAGCATTGTGAGTGTAACGGCCTACAT 2419
          | |      | | | | | | | | | | | | | | | | | | | | | |
Db      346  CACGCTGATCATGCTGCTTTCCCTGGCAGCTTTTCAGTGTTCATCAGTGTGGTTTCTTACCT 405

Qy      2420 TGCCTTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAAGGGTGTGATCCAGGC 2479
          | | | | | | | | | | | | | | | | | | | | | | |

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Db 406 CATCCTGGCTCTTCTCTCTGTCACCATCAGCTTCAGGATCTACAAGTCCGTCATCCAAGC 465
 Qy 2480 TATCCAGAAATCTGATGAAGGCCACCCATTCAGGGCATATTTGGAATCTGAAGTTGCTAT 2539
 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db 466 TGTACAGAAGTCAGAAGAAGGCCATCCATTCAAAGCCTACCTGGACGTAGACATTACTCT 525
 Qy 2540 ATCTGAGGAGTTGGTTTCAGAAGTACAGCAATTCTGCTCTTGGTCATGTTAACTGCACAAT 2599
 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db 526 GTCCTCAGAAGCTTTCCATAATTACATGAATGCTGCCATGGTGCACATCAACAGGGCCCT 585
 Qy 2600 AAAAGAACTCAGACGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGT 2659
 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db 586 GAAACTCATTATTCGTCTCTTCTGGTAGAAGATCTGGTTGACTCCTTGAAGCTGGCTGT 645
 Qy 2660 GTTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTCATGGTCTGACACTACTAATTTT 2719
 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db 646 CTTTCATGTGGCTGATGACCTATGTTGGTGGCTGTTTTTAACGGAATCACCCCTTCTAATTCT 705
 Qy 2720 GGCTCTGATTTCACTCTTCAGTGTTCCCTGTTATTTATGAACGGCATCAGGCGCAAATAGA 2779
 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db 706 TGCTGAACTGCTCATTTCAGTGTCCTGATTGTCTATGAGAAGTACAAGACCCAGATTGA 765
 Qy 2780 TCATTATCTGGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAA 2839
 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db 766 TCACTATGTTGGCATCGCCCGAGATCAGACCAAGTCAATTGTTGAAAAGATCCAAGCAAA 825
 Qy 2840 AATCCCTGGATT 2851
 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db 826 ACTCCCTGGAAT 837

RESULT 7

US-09-149-476-255

; Sequence 255, Application US/09149476

; Patent No. 6420526

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: 186 Human Secreted proteins

; FILE REFERENCE: PZ002P1

; CURRENT APPLICATION NUMBER: US/09/149,476

; CURRENT FILING DATE: 1998-09-08

; EARLIER APPLICATION NUMBER: PCT/US98/04493

; EARLIER FILING DATE: 1998-03-06

; EARLIER APPLICATION NUMBER: 60/040,162

; EARLIER FILING DATE: 1997-03-07

; EARLIER APPLICATION NUMBER: 60/040,333

; EARLIER FILING DATE: 1997-03-07

; EARLIER APPLICATION NUMBER: 60/038,621

; EARLIER FILING DATE: 1997-03-07

; EARLIER APPLICATION NUMBER: 60/040,626

; EARLIER FILING DATE: 1997-03-07

; EARLIER APPLICATION NUMBER: 60/040,334

; EARLIER FILING DATE: 1997-03-07

; EARLIER APPLICATION NUMBER: 60/040,336

; EARLIER FILING DATE: 1997-03-07

; EARLIER APPLICATION NUMBER: 60/040,163

; EARLIER FILING DATE: 1997-03-07

; EARLIER APPLICATION NUMBER: 60/047,600
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,615
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,597
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,502
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; EARLIER FILING DATE: 1997-08-22

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; EARLIER APPLICATION NUMBER: 60/057,669

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 ; EARLIER APPLICATION NUMBER: 60/049,610
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 ; EARLIER APPLICATION NUMBER: 60/061,060
 ; EARLIER FILING DATE: 1997-10-02

Query Match 6.0%; Score 230.4; DB 4; Length 2664;
 Best Local Similarity 63.6%; Pred. No. 2.2e-48;
 Matches 351; Conservative 0; Mismatches 201; Indels 0; Gaps 0;

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Db      321  CACGCTGATCATGCTGCTTTCCCTGGCAGCTTTTCAGTGTTCATCAGTGTGGTTTCTTACCT 380

Qy      2420 TGCCTTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAAGGGTGTGATCCAGGC 2479
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Db      381  CATCCTGGCTCTTCTCTCTGTGACCATCAGCTTCAGGATCTACAAGTCCGTATCCAAGC 440

Qy      2480 TATCCAGAAATCTGATGAAGGCCACCCATTTCAGGGCATATTTGGAATCTGAAGTTGCTAT 2539
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Qy      2660 GTTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTCAATGGTCTGACACTACTAATTTT 2719
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Db      681  TGCTGAACTGCTCATTTTCAGTGTCCCGATTGTCTATGAGAAGTACAAGACCCAGATTGA 740

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Qy      2840 AATCCCTGGATT 2851
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Db      801  ACTCCCTGGAAT 812
  
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RESULT 8

US-08-700-607-4

; Sequence 4, Application US/08700607

; Patent No. 5858708

; GENERAL INFORMATION:

; APPLICANT: Bandman, Olga


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; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,607
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0114 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 4:
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; MOLECULE TYPE: cDNA
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US-08-700-607-4

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; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0114 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 9:
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; STRANDEDNESS: single
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; CLONE: 28742
US-08-700-607-9

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Qy      2423 CTTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAAGGGTGTGATCCAGGCTAT 2482
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Qy      2543 TGAGGAGTTGGTTCAGAAGTACA 2565
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; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise

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; APPLICANT: Jiang Yuqui
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C9
; CURRENT APPLICATION NUMBER: US/09/439,313
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 279
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(301)
; OTHER INFORMATION: n = A,T,C or G
US-09-439-313-279
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Qy      3374 TGTTGTATTAATTGCCAATATAAGTAAATATAGATTATATATATCTATATATAGTGTTTC 3433
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Db      60 TGTTATATTAATTGCCAATATAAGTAAATATAGATTATA-----TATGTATAGTGTTTC 113

Qy      3434 ACGAAGCTTAGCCCTTTACCTTCCCAGCTGCCCCACAGTGCTTGATACT-----TCTGT 3487
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Db      114 ACAAAGCTTAGACCTTTACCTT-CCAGCCACCCACAGTGCTTGATATTTTACAGAGTCAGT 172

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Qy      3607 ACTTCACTGCACAGA 3621
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RESULT 12
US-09-352-616A-279
; Sequence 279, Application US/09352616A
; Patent No. 6395278
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; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang, Yuqui
; APPLICANT: Xu, Jiangchun
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.427C8
; CURRENT APPLICATION NUMBER: US/09/352,616A
; CURRENT FILING DATE: 1999-07-13
; NUMBER OF SEQ ID NOS: 472
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 279
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(301)
; OTHER INFORMATION: n = A,T,C or G
US-09-352-616A-279
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Query Match          3.6%; Score 138.6; DB 4; Length 301;
Best Local Similarity 80.3%; Pred. No. 1.3e-25;
Matches 253; Conservative 0; Mismatches 41; Indels 21; Gaps 7;
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Qy      3607 ACTTCACTGCACAGA 3621
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Db      287 ATTCATTGCACAGA 301
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RESULT 13
US-09-232-149A-279
; Sequence 279, Application US/09232149A
; Patent No. 6465611
; GENERAL INFORMATION:
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; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
; TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.427C6
; CURRENT APPLICATION NUMBER: US/09/232,149A
; CURRENT FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 338
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 279
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(301)
; OTHER INFORMATION: n = A,T,C or G
US-09-232-149A-279
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Query Match          3.6%; Score 138.6; DB 4; Length 301;
Best Local Similarity 80.3%; Pred. No. 1.3e-25;
Matches 253; Conservative 0; Mismatches 41; Indels 21; Gaps 7;
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RESULT 14

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; Sequence 279, Application US/09159812A
; Patent No. 6613872
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF
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; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.42717C17
; CURRENT APPLICATION NUMBER: US/09/636,215
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 852
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 279
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(301)
; OTHER INFORMATION: n = A,T,C or G
US-09-636-215-279
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Best Local Similarity 80.3%; Pred. No. 1.3e-25;
Matches 253; Conservative 0; Mismatches 41; Indels 21; Gaps 7;
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Perfect score: 3833
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Listing first 45 summaries

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- 19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2649.8	69.1	4632	15	US-10-060-036-53	Sequence 53, Appl
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3	2379.4	62.1	4053	9	US-09-972-599A-5	Sequence 5, Appli
4	2379.4	62.1	4053	17	US-10-717-597-310	Sequence 310, Appl
5	2223.6	58.0	3579	9	US-09-789-386-1	Sequence 1, Appli
6	2223.6	58.0	3579	9	US-09-893-348-22	Sequence 22, Appl
7	2223.6	58.0	3579	12	US-10-267-502-212	Sequence 212, App
8	2223.6	58.0	3579	17	US-10-327-213-8	Sequence 8, Appli
9	2223.6	58.0	3579	17	US-10-466-258-8	Sequence 8, Appli
10	2179.4	56.9	4684	9	US-09-893-348-17	Sequence 17, Appl
11	1866	48.7	3492	12	US-10-267-502-214	Sequence 214, App
12	1414.6	36.9	1980	16	US-10-220-891-22	Sequence 22, Appl
13	1025.4	26.8	2235	15	US-10-060-036-54	Sequence 54, Appl
14	989.2	25.8	1514	13	US-09-823-245A-349	Sequence 349, App
15	986	25.7	1798	17	US-10-466-258-10	Sequence 10, Appl
16	915.6	23.9	1785	16	US-10-439-388-62	Sequence 62, Appl
17	827.2	21.6	2052	17	US-10-466-258-3	Sequence 3, Appli
18	826.4	21.6	2782	15	US-10-205-194-165	Sequence 165, App
19	789.8	20.6	2610	17	US-10-641-643-382	Sequence 382, App
20	685.8	17.9	1610	9	US-09-765-205-5	Sequence 5, Appli
21	683	17.8	1160	15	US-10-175-523-156	Sequence 156, App
22	681.4	17.8	994	12	US-09-978-360A-110	Sequence 110, App
23	590.8	15.4	799	13	US-10-660-946-2	Sequence 2, Appli
24	538.8	14.1	868	9	US-09-789-386-3	Sequence 3, Appli
c 25	535	14.0	4710	10	US-09-764-891-7385	Sequence 7385, Ap
26	527	13.7	1122	9	US-09-789-386-5	Sequence 5, Appli
27	484.6	12.6	972	16	US-10-437-931-1	Sequence 1, Appli
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31	427	11.1	441	9	US-09-983-965-3801	Sequence 3801, Ap
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35	400.4	10.4	566	13	US-10-085-783A-17576	Sequence 17576, A
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41	337.4	8.8	3413	14	US-10-001-843-61	Sequence 61, Appl
c 42	316.6	8.3	3413	14	US-10-001-843-61	Sequence 61, Appl
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ALIGNMENTS

RESULT 1
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 ; Sequence 53, Application US/10060036
 ; Publication No. US20030073144A1
 ; GENERAL INFORMATION:

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; APPLICANT: Benson, Darin R.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Persing, David H.
; APPLICANT: Heppler, William T.
; APPLICANT: Jiang, Yugu
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
; FILE REFERENCE: 210121.566
; CURRENT APPLICATION NUMBER: US/10/060,036
; CURRENT FILING DATE: 2002-01-30
; NUMBER OF SEQ ID NOS: 4560
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 53
; LENGTH: 4632
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-036-53
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Matches 3292; Conservative 0; Mismatches 442; Indels 137; Gaps 24;
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Qy	1557	GAAGTTCCACAAAAACAAGATGAAGCTGTAATACTTGTGAAAGAAAACCTCACTGAAATT	1616
Db	2404	GACGTTCCACAAAAACAAGATGAAACTGTGATGCTTGTGAAAGAAAGTCTCACTGAGACT	2463
Qy	1617	TCATCTGAGTCAATGACAGGACATGACAATAAGGGAAAACCTCAGTGCTTCACCATCACCT	1676
Db	2464	TCATTTGAGTCAATGATAGAATATGAAAATAAGGAAAAACCTCAGTGCTTTGC---CACCT	2520
Qy	1677	GAGGGAGGAAAACCGTATTTGGAGTCTTTTCAGCCCAGTTTAGGCATCACAAAAGATACC	1736
Db	2521	GAGGGAGGAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATACC	2580
Qy	1737	TTAGCACCTGATGAAGTTTCAGCATTGACCCAAAAGGAGAAAATCCCTTTGCAGATGGAG	1796
Db	2581	CTGTTACCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAATTCCTTTGCAGATGGAG	2640
Qy	1797	GAGCTCAATACTGCAGTTTATTCAAGTGATGGCTTATTCATTGCTCAGGAAGCAAACCTA	1856
Db	2641	GAGCTCAGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGATA	2700
Qy	1857	AGAGAAAGTGAAACATTTTCAGATTTCATCTCCGATTGAGATTATAGATGAGTTCCCGACC	1916
Db	2701	AGAGAAACTGAAACGTTTTCAGATTTCATCTCCAATTGAAATTATAGATGAGTTCCCTACA	2760
Qy	1917	TTTGTCAGTTCTAAAGCAGATTCTTCTCCTACATTAGCCAGGGAATACACTGACCTAGAA	1976
Db	2761	TTGATCAGTTCTAAAACTGATTCAATTTCTAAATTAGCCAGGGAATATACTGACCTAGAA	2820
Qy	1977	GTAGCCACAAAAGTGAAATTGCTGACATCCAGGATGGAGCTGGGTCATTGGCTTGTGCA	2036
Db	2821	GTATCCACAAAAGTGAAATTGCTAATGCCCCGGATGGAGCTGGGTCATTGCCTTGCACA	2880
Qy	2037	GGATTGCCCCATGACCTTTCTTTCAAGAGTATACAACC-----TAAAGAGGAAGTTCAT	2090
Db	2881	GAATTGCCCCATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCAGT	2940
Qy	2091	GTCCAGATGAGTTCTCCAAAGATAGGGGTGATGTTTCAAAGGTGCCCGTACTGCCTCCA	2150
Db	2941	TTCTCAGATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCA	3000
Qy	2151	GATGTTTCTGCTTTGGATGCTCAAGCAGAGATAGGCAGCATAGAAAAACCCAAAGTTCTT	2210
Db	3001	GATGTTTCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTT	3060

Qy	2211	GTGAAAGAAGCCGAGAGAAAACCTTCCTTCTGATACAGAAAAAGAGCGAAGATCTCCATCT	2270
Db	3061	GTGAAAGAAGCTGAGAAAAACCTTCCTTCCGATACAGAAAAAGAGGACAGATCACCATCT	3120
Qy	2271	GCTATATTTTCAGCAGAGCTGAGTAAACCTTCAGTTGTTGACCTCCTCTACTGGAGAGAC	2330
Db	3121	GCTATATTTTCAGCAGAGCTGAGTAAACCTTCAGTTGTTGACCTCCTGTACTGGAGAGAC	3180
Qy	2331	ATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCTTGTTTCCTGCTGCTCTCGCTGACAGTA	2390
Db	3181	ATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCCTATTCCTGCTGCTTTCATTGACAGTA	3240
Qy	2391	TTCAGCATTGTGAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCTGTGACTATCAGC	2450
Db	3241	TTCAGCATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGC	3300
Qy	2451	TTTAGGATATATAAGGGTGTGATCCAGGCTATCCAGAAATCTGATGAAGGCCACCCATTC	2510
Db	3301	TTTAGGATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTC	3360
Qy	2511	AGGGCATATTTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGCAAT	2570
Db	3361	AGGGCATATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGTAAT	3420
Qy	2571	TCTGCTCTTGGTCATGTTAACTGCACAATAAAAGAACTCAGACGCCTCTTCTTAGTTGAT	2630
Db	3421	TCTGCTCTTGGTCATGTGAAGTGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGAT	3480
Qy	2631	GATTTAGTTGATTCTCTGAAGTTTGAGTGTGATGTGGGTATTTACCTATGTTGGTGCC	2690
Db	3481	GATTTAGTTGATTCTCTGAAGTTTGAGTGTGATGTGGGTATTTACCTATGTTGGTGCC	3540
Qy	2691	TTGTTCAATGGTCTGACACTACTAATTTTGGCTCTGATTTCACTCTTCAGTGTTCTGTT	2750
Db	3541	TTGTTTAAATGGTCTGACACTACTGATTTTGGCTCTCATTTCACCTCTTCAGTGTTCTGTT	3600
Qy	2751	ATTTATGAACGGCATCAGGCGCAAATAGATCATTATCTGGGACTTGCAAATAAGAATGTT	2810
Db	3601	ATTTATGAACGGCATCAGGCACAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTT	3660
Qy	2811	AAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGAATGA	2870
Db	3661	AAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGAATGA	3720
Qy	2871	GAAAGCCTGAAAGAGTTAACAATAGAGGAGTTTATCTTTAAAGGGGATATTCATTTGATT	2930
Db	3721	AAACGCCCAAAATAATTAGT-----AGGAGTTCATCTTTAAAGGGGATATTCATTTGATT	3775
Qy	2931	CCATTGGGGAGGGTCAGGGAAGAACAAGCCTTGACATTGCAGTGCAGTTTCACAGATCT	2990
Db	3776	AT-----ACGGATCT	3785
Qy	2991	TTATTTTCTAGCAACGCAGTG-TCTGAGGAAAAATGACCTGTCTTGACTGCCCTGTGTTCA	3049
Db	3786	TTATTTTCTAGCCATGCACTGTTGTGAGGAAAAATTACCTGTCTTGACTGCCATGTGTTCA	3845
Qy	3050	TCATCTTAAGTATTGTAAGCTGCTATGTATGGATTAAATCGTAATCATATTTGTTTTTC	3109

Db	3846	TCATCTTAAGTATTGTAAGCTGCTATGTATGGATTAAACCGTAATCATA--TCTTTTTTC	3903
Qy	3110	CTGTATGAGGCACTGGTGAATAAAACAAAGATCTGAGAAAGCTGTATATTACACTTTGTCG	3169
Db	3904	CTATCTGAGGCACTGGTGGA-----ATAAAAACCTGTATATTTACTTTGTTG	3952
Qy	3170	CAGGTAGTCTTGCTGTAT-TTGGGGAATTGCAAAGAAAGTGGAGCT-----GACAGAAA	3222
Db	3953	CAGATAGTCTTGCCGCATCTTGGCAAGTTCAGAGATGGTGGAGCTAGAAAAAAAAAAAAA	4012
Qy	3223	TAACCCTTTTCACAGTTTGTGCACTGTGTACGGTCTGTGTAGGTTGATGCAGATTTTCTG	3282
Db	4013	AAAAGCCCTTTTCAGTTTGTGCACTGTGTATGGTCCGTGTAGATTGATGCAGATTTTCTG	4072
Qy	3283	AAATGAAA----TGTTTAGACGAGATCATGCCACCAAGGCAGGAGTGAAAAAGCTTGCCCT	3338
Db	4073	AAATGAAATGTTTGTTTAGACGAGATCATACCGGTAAAGCAGGAATGACAAAGCTTG-CT	4131
Qy	3339	TTCCTGGTATGTTCTAGGTGTATTGTGAAATTTACTGTTGTATTAATTGCCAATATAAGT	3398
Db	4132	TTTCTGGTATGTTCTAGGTGTATTGTGACTTTTACTGTTATATTAATTGCCAATATAAGT	4191
Qy	3399	AAATATAGATTATATATATCTATATATAGTGTTCACGAAGCTTAGCCCTTTACCTTCCC	3458
Db	4192	AAATATAGATTATATATG-----TATAGTGTTCACAAAGCTTAGACCTTTACCTT-CC	4244
Qy	3459	AGCTGCCCCACAGTGCTTGATACT-----TCTGTCATGGGTTTATGTGTGTAGTCCCA	3512
Db	4245	AGCCACCCCACAGTGCTTGATATTTAGAGTCAGTCATTGGTTATACATGTGTAGTTCCA	4304
Qy	3513	AAGCACATAAGCTAGGGAGAAACGTACTTCTAGGCGCACTACCATCTGTTTTCAACACGA	3572
Db	4305	AAGCACATAAGCTAGAAGAAGAAATATTTCTAGGAGCACTACCATCTGTTTTCAACATGA	4364
Qy	3573	ACCGACGCCATGCAAACAGAACTCC-TCAACATAAACTTCACTGCACAGACTTACTGTAG	3631
Db	4365	A---ATGCCACACACATAGAACTCCAACAACATCAATTTCACTGCACAGACTGACTGTAG	4421
Qy	3632	TTAATTTTATCAC--AAACTCTGGACTGAATCTAATGCTTCCAAAAA-----TGTTTG	3682
Db	4422	TTAATTTTGTACAGAATCTATGGACTGAATCTAATGCTTCCAAAAATGTTGTTTGTGTTG	4481
Qy	3683	CAAATATCAAACATTGTTATGTAAGAAAATAT-----AAATGACGATTATACAATT	3734
Db	4482	CAAATATCAAACATTGTTATGCAAGAAATTTATTAATTACAAAATGAAGATTATACCATT	4541
Qy	3735	GTGGTTTAAGCTGTATTGAACTAAATCTGTGGAATGCATTGTGAACTGTAAAAGCAAAGT	3794
Db	4542	GTGGTTTAAGCTGTACTGAACTAAATCTGTGGAATGCATTGTGAACTGTAAAAGCAAAGT	4601
Qy	3795	ATCAATAAAGCTTATAGACTTAAAAAAAAAAAA	3825
Db	4602	ATCAATAAAGCTTATAGACTTAAAAAAAAAAAA	4632

US-09-758-140-5
; Sequence 5, Application US/09758140
; Patent No. US20020012965A1
; GENERAL INFORMATION:
; APPLICANT: Strittmatter, Stephen M.
; TITLE OF INVENTION: No. US20020012965A1o Receptor-Mediated Blockade of
Axonal Growth
; FILE REFERENCE: 44574-5073-US
; CURRENT APPLICATION NUMBER: US/09/758,140
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/175,707
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: US 60/207,366
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,378
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 4053
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (135)..(3710)
; OTHER INFORMATION: Human mRNA for No. US20020012965A1o protein (KIAA0886,
GenBank
; OTHER INFORMATION: Accession No. US20020012965A1 AB020693)
US-09-758-140-5

Query Match 62.1%; Score 2379.4; DB 9; Length 4053;
Best Local Similarity 86.6%; Pred. No. 0;
Matches 2802; Conservative 0; Mismatches 381; Indels 54; Gaps 14;

Qy	1	CTATCTCCTCTCTCAGCCGCTGCTTTTAAAGAACGTGAATACCTTGGTGATTTACCAGCA	60
Db	846	CTGTCTCCTCTCTCAGCCGCTTCTTTCAAAGAACATGAATACCTTGGTAATTTGTCAACA	905
Qy	61	GTACTGCCCCACTGAAGGAACACTTCCAGCAACTTCAAATGAAGCTTCTAAAGCATTCTCA	120
Db	906	GTATTACCCACTGAAGGAACACTTCAAGAAAATGTCAGTGAAGCTTCTAAAGAGGTCTCA	965
Qy	121	GAGAAGGCAAAAAATCCATTTGTAGAGAGAAATTTAACAGAATTTTCAGAATTGGAATAT	180
Db	966	GAGAAGGCAAAAACTCTACTCATAGATAGAGATTTAACAGAGTTTTTCAGAATTAGAATAC	1025
Qy	181	TCAGAAATGGAATCATCATTTCAGTGGCTCTCAAAGGCAGAACCTGCCGTAACAGTAGCG	240
Db	1026	TCAGAAATGGGATCATCGTTTCAGTGTCTCTCCAAAAGCAGAAATCTGCCGTAATAGTAGCA	1085
Qy	241	AATCCTAGGGACGAAATAGTTGTGAGGAGTAGAGATAAAGAAGAGGACTTAGTTAGTCTT	300
Db	1086	AATCCTAGGGAAGAAATAATCGTGAAAAATAAGATGAAGAAGAGAAGTTAGTTAGTAAT	1145
Qy	301	AACATCCTTCATACTCAGCAGGAGTTATCTACAGTCCTTACGAAATCAGTTGAAGAAGAA	360
Db	1146	AACATCCTTCATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGGTTAAAGAGGAT	1205

Qy	361	GATAGAGTTCTGTCTCCAGAAAAACAAAGGCAGTTTTAAAGGAAAAGGGAGTTGCAGCA	420
Db	1206	GA---AGTTGTGTCTTCAGAAAAAGCAAAAGACAGTTTAAATGAAAAGAGAGTTGCAGTG	1262
Qy	421	GAAGCTTCTATGGGGGAGGAATATGCAGACTTCAAACCATTGAGCGAGTATGGGAAGTG	480
Db	1263	GAAGCTCCTATGAGGGAGGAATATGCAGACTTCAAACCATTGAGCGAGTATGGGAAGTG	1322
Qy	481	AAAGATACTTACAAGCAAGATAGTGATGTTTGTATTGCTGGAGGTAATATAGAGAGCAAA	540
Db	1323	AAAGATAGT---AAGGAAGATAGTGATATGTTGGCTGCTGGAGGTAATAATCGAGAGCAAC	1379
Qy	541	TTGGAAGGTAAAGTGGATAAGAAACACTTTTCAGATAGCCTTGAACAAACAAATCGTGAA	600
Db	1380	TTGGAAGGTAAAGTGGATAAAAAATGTTTTCAGATAGCCTTGAACAAACAAATCGTGAA	1439
Qy	601	AAAGATAGTGAAAGCAGTAATGATGACACTTCATTTCCCAGTACACCAGAAGCTGTAAGA	660
Db	1440	AAAGATAGTGAGAGTAGTAATGATGATACTTCTTTCCCCAGTACGCCAGAAGGTATAAAG	1499
Qy	661	GGTGGTTCCGGAGCGTACATCACGTGTGCTCCCTTTAACC---CAACAAGTGAAGTGT	717
Db	1500	GATCGTTCCAGGAGCATATATCACATGTGCTCCCTTTAACCAGCAGCAACTGAGAGCATT	1559
Qy	718	TCAACAAACATTTTTCCCTTGTTGGAAGATCATACTTCGGAAAATAAGACAGATGAAAAA	777
Db	1560	GCAACAAACATTTTTCCCTTGTTAGGAGATCCTACTTCAGAAAATAAGACCGATGAAAAA	1619
Qy	778	AAGATAGAA-AAAAAAGGCACAAATTGTAACAGAGAAGAATGCAAGTGTCAAGACATCA	836
Db	1620	AAAATAGAAGAAAAGAAGGCCAAATAGTAACAGAGAAGAATACTAGCACCAAACATCA	1679
Qy	837	AACCCTTTCTTTATGGCAGCACAGGAGTCTAAGACAGATTACGTTACAACAGATCATGTG	896
Db	1680	AACCCTTTCTTTGTAGCAGCACAGGATTCTGAGACAGATTATGTCACAACAGATAATTTA	1739
Qy	897	TCAAAGGTGACCGAGGAAGTAGTGGCAAACATGCCTGAAGGTCTAACCCAGATTTGGTT	956
Db	1740	ACAAAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCCAGATTTAGTA	1799
Qy	957	CAGGAAGCATGTGAAAGTGAATTGAATGAAGCTACTGGTACAAAAATTGCCTTTGAAACA	1016
Db	1800	CAGGAAGCATGTGAAAGTGAATTGAATGAAGTTACTGGTACAAAGATTGCTTATGAAACA	1859
Qy	1017	AAAATGGACCTGGTTCAAACCTTCAGAAGCTGTGCAGGAGTCACTTTACCCTGTAACACAG	1076
Db	1860	AAAATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCACAG	1919
Qy	1077	CTTTGCCCATCTTTTGAAGAATCTGAAGCTACTCCGTCACCGGTTTTGCCTGACATTGTC	1136
Db	1920	CTTTGCCCATCATTTGAAGAGTCAGAAGCTACTCCTTCACAGTTTTGCCTGACATTGTT	1979
Qy	1137	ATGGAAGCACCATTAAATTCTGTAGTTCCTAGTGCTGGTGCTTCTGCAGTGCAGCTCAGT	1196
Db	1980	ATGGAAGCACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTTGATACAGCCCAGC	2039

Qy	1197	TCATCACCATTAGAACTCTTCCTTCAGTTAATTATGAAAGCATAAAGTTTGGAGCCTGAA	1256
Db	2040	TCATCACCATTAGAAGC---TTCTTCAGTTAATTATGAAAGCATAAAACATGAGCCTGAA	2096
Qy	1257	AATCCCCCACCATATGAGGAGGCCATGAATGTATCACTAAAAAAGAATCAGGAATGAAT	1316
Db	2097	AACCCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAGTATCAGGAATAAAG	2156
Qy	1317	GAAGAAATCACAGAGCCTGAAGGTATTAGTGTAGCTGTTTCAGGAAACAGAAGCTCCTTAT	1376
Db	2157	GAAGAAATTAAAGAGCCTGAAAATATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTAT	2216
Qy	1377	ATATCTATTGCATGTGATTTAATTAAAGAAACAAAGATCTCTACTGAACCGACTCCAGAT	1436
Db	2217	ATATCTATTGCATGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAACCAGCTCCGGAT	2276
Qy	1437	TTCTCTAGTTATTCAGAAATAGCAGAAGTTGCACAGCCAGTGCCCCGAGCATTCTGAGCTA	1496
Db	2277	TTCTCTGATTATTCAGAAATGGCAAAAGTTGAACAGCCAGTGCCCTGATCATTCTGAGCTA	2336
Qy	1497	GTTGAAGATTCCCTCCCCGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCC	1556
Db	2337	GTTGAAGATTCCCTCACCTGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCT	2396
Qy	1557	GAAGTTCCACAAAAACAAGATGAAGCTGTAATACTTGTGAAAGAAAACCTCACTGAAATT	1616
Db	2397	GACGTTCCACAAAAACAAGATGAAACTGTGATGCTTGTGAAAGAAAGTCTCACTGAGACT	2456
Qy	1617	TCATCTGAGTCAATGACAGGACATGACAATAAGGGAAAACTCAGTGCTTCACCATCACCT	1676
Db	2457	TCATTTGAGTCAATGATAGAATATGAAAATAAGGAAAACTCAGTGCTTTGC---CACCT	2513
Qy	1677	GAGGGAGGAAAACCGTATTTGGAGTCTTTTCAGCCAGTTTAGGCATCACAAAAGATAACC	1736
Db	2514	GAGGGAGGAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATAACC	2573
Qy	1737	TTAGCACCTGATGAAGTTTCAGCATTGACCCAAAAGGAGAAAATCCCTTTGCAGATGGAG	1796
Db	2574	CTGTTACCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAATTCCTTTGCAGATGGAG	2633
Qy	1797	GAGCTCAATACTGCAGTTTATTCAAGTGATGGCTTATTCATTGCTCAGGAAGCAAACCTA	1856
Db	2634	GAGCTCAGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGATA	2693
Qy	1857	AGAGAAAGTGAAACATTTTCAGATTTCATCTCCGATTGAGATTATAGATGAGTTCCCGACC	1916
Db	2694	AGAGAAACTGAAACGTTTTCAGATTTCATCTCCAATTGAAATTATAGATGAGTTCCCTACA	2753
Qy	1917	TTTGTGAGTTCTAAAGCAGATTCTTCTCTACATTAGCCAGGGAATACACTGACCTAGAA	1976
Db	2754	TTGATCAGTTCTAAAACTGATTCAATTTCTAAATTAGCCAGGGAATATACTGACCTAGAA	2813
Qy	1977	GTAGCCACAAAAGTGAAATTGCTGACATCCAGGATGGAGCTGGGTTCATTGGCTTGTGCA	2036
Db	2814	GTATCCACAAAAGTGAAATTGCTAATGCCCCGGATGGAGCTGGGTTCATTGCCTTGCACA	2873
Qy	2037	GGATTGCCCCATGACCTTTCTTTCAAGAGTATACAACC-----TAAAGAGGAAGTTCAT	2090

Db	2874	GAATTGCCCCATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCAGT	2933
Qy	2091	GTCCCAGATGAGTTCTCCAAAGATAGGGGTGATGTTTCAAAGGTGCCCCGACTGCCTCCA	2150
Db	2934	TTCTCAGATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCA	2993
Qy	2151	GATGTTTCTGCTTTGGATGCTCAAGCAGAGATAGGCAGCATAGAAAAACCCAAAGTTCTT	2210
Db	2994	GATGTTTCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTT	3053
Qy	2211	GTGAAAGAAGCCGAGAGAAAACTTCCTTCTGATACAGAAAAAGAGCGAAGATCTCCATCT	2270
Db	3054	GTGAAAGAAGCTGAGAAAAAACTTCCTTCCGATACAGAAAAAGAGGACAGATCACCATCT	3113
Qy	2271	GCTATATTTTTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGAC	2330
Db	3114	GCTATATTTTTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTGTACTGGAGAGAC	3173
Qy	2331	ATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCTTGTTTCTGCTGCTCTCGCTGACAGTA	2390
Db	3174	ATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCCTATTCTGCTGCTTTTCATTGACAGTA	3233
Qy	2391	TTCAGCATTGTGAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCTGTGACTATCAGC	2450
Db	3234	TTCAGCATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGC	3293
Qy	2451	TTTAGGATATATAAGGGTGTGATCCAGGCTATCCAGAAATCTGATGAAGGCCACCCATTC	2510
Db	3294	TTTAGGATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTC	3353
Qy	2511	AGGGCATATTTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTTCAGAAGTACAGCAAT	2570
Db	3354	AGGGCATATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTTCAGAAGTACAGTAAT	3413
Qy	2571	TCTGCTCTTGGTCATGTAACTGCACAATAAAAGAACTCAGACGCCTCTTCTTAGTTGAT	2630
Db	3414	TCTGCTCTTGGTCATGTGAAGTGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGAT	3473
Qy	2631	GATTTAGTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCC	2690
Db	3474	GATTTAGTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCC	3533
Qy	2691	TTGTTCAATGGTCTGACACTACTAATTTTGGCTCTGATTTCACTCTTCAGTGTTCTGTT	2750
Db	3534	TTGTTTAATGGTCTGACACTACTGATTTTGGCTCTCATTTCCTCAGTGTTCTGTT	3593
Qy	2751	ATTTATGAACGGCATCAGGCGCAAATAGATCATTATCTGGGACTTGCAAATAAGAATGTT	2810
Db	3594	ATTTATGAACGGCATCAGGCACAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTT	3653
Qy	2811	AAAGATGCTATGGCTAAAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGAATGA	2870
Db	3654	AAAGATGCTATGGCTAAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCTGAATGA	3713
Qy	2871	GAAAGCCTGAAAGAGTTAACAATAGAGGAGTTTATCTTTAAAGGGGATATTCATTTGATT	2930

Query Match 62.1%; Score 2379.4; DB 9; Length 4053;
Best Local Similarity 86.6%; Pred. No. 0;
Matches 2802; Conservative 0; Mismatches 381; Indels 54; Gaps 14;

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Qy      1 CTATCTCCTCTCTCAGCCGCTGCTTTTAAAGAACGTGAATACCTTGGTGATTACCAGCA 60
      || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    846 CTGTCTCCTCTCTCAGCCGCTTCTTTCAAAGAACATGAATACCTTGGTAATTTGTCAACA 905

Qy     61 GTACTGCCCCACTGAAGGAACACTTCCAGCAACTTCAAATGAAGCTTCTAAAGCATTCTCA 120
      ||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    906 GTATTACCCACTGAAGGAACACTTCAAGAAAATGTCAGTGAAGCTTCTAAAGAGGTCTCA 965

Qy    121 GAGAAGGCAAAAAATCCATTTGTAGAGAGAAATTTAACAGAATTTTCAGAATTGGAATAT 180
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    966 GAGAAGGCAAAAACTCTACTCATAGATAGAGATTTAACAGAGTTTTCAGAATTAGAATAC 1025

Qy    181 TCAGAAATGGAATCATCATTTCAGTGGCTCTCAAAAGGCAGAACCTGCCGTAACAGTAGCG 240
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db   1026 TCAGAAATGGGATCATCGTTTCAGTGTCTCTCCAAAAGCAGAACTCTGCCGTAATAGTAGCA 1085

Qy    241 AATCCTAGGGACGAAATAGTTGTGAGGAGTAGAGATAAAGAAGAGGACTTAGTTAGTCTT 300
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db   1086 AATCCTAGGGAAGAAATAATCGTGAAAAATAAAGATGAAGAAGAGAAGTTAGTTAGTAAT 1145

Qy    301 AACATCCTTCATACTCAGCAGGAGTTATCTACAGTCCTTACGAAATCAGTTGAAGAAGAA 360
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db   1146 AACATCCTTCATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGGTTAAAGAGGAT 1205

Qy    361 GATAGAGTTCTGTCTCCAGAAAAAACAAAGGACAGTTTTTAAGGAAAAGGGAGTTGCAGCA 420
      || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db   1206 GA---AGTTGTGTCTTCAGAAAAAGCAAAGACAGTTTTTAATGAAAAGAGAGTTGCAGTG 1262

Qy    421 GAAGCTTCTATGGGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTG 480
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db   1263 GAAGCTCCTATGAGGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTG 1322

Qy    481 AAAGATACTTACAAGCAAGATAGTGATGTTTTGATTGCTGGAGGTAATATAGAGAGCAAA 540
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db   1323 AAAGATAGT---AAGGAAGATAGTGATATGTTGGCTGCTGGAGGTAATATCGAGAGCAAC 1379

Qy    541 TTGGAAGGTAAAGTGGATAAGAAACACTTTTCAGATAGCCTTGAACAAACAAATCGTGAA 600
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db   1380 TTGGAAGGTAAAGTGGATAAAAAATGTTTTGCAGATAGCCTTGAACAAACTAATCACGAA 1439

Qy    601 AAAGATAGTGAAAGCAGTAATGATGACACTTCATTTCCAGTACACCAGAAGCTGTAAGA 660
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db   1440 AAAGATAGTGAGAGTAGTAATGATGATACTTCTTTCCCGAGTACGCCAGAAGGTATAAAG 1499

Qy    661 GGTGGTTCCGGAGCGTACATCACGTGTGCTCCCTTTAACC---CAACAAGTGAAGTGT 717
      || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db   1500 GATCGTTCAGGAGCATATATCACATGTGCTCCCTTTAACCCAGCAGCAACTGAGAGCATT 1559

Qy    718 TCAACAAACATTTTTCCCTTGTGGAAGATCATACTTCGGAAAATAAGACAGATGAAAAA 777
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db   1560 GCAACAAACATTTTTCCCTTGTAGGAGATCCTACTTCAGAAAATAAGACCGATGAAAAA 1619

Qy    778 AAGATAGAA-AAAAAAGGCACAAATTGTAACAGAGAAGAATGCAAGTGCAAGACATCA 836
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Db	1620	AAAATAGAAGAAAAGAAGGCCCAAATAGTAACAGAGAAGAATACTAGCACCAAAACATCA	1679
Qy	837	AACCCCTTTCCTTATGGCAGCACAGGAGTCTAAGACAGATTACGTTACAACAGATCATGTG	896
Db	1680	AACCCCTTTCCTTGTAGCAGCACAGGATTCTGAGACAGATTATGTCACAACAGATAATTTA	1739
Qy	897	TCAAAGGTGACCGAGGAAGTAGTGGCAAACATGCCTGAAGGTCTAACCCCAGATTTGGTT	956
Db	1740	ACAAAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCCAGATTTAGTA	1799
Qy	957	CAGGAAGCATGTGAAAGTGAATTGAATGAAGCTACTGGTACAAAAATTGCCTTTGAAACA	1016
Db	1800	CAGGAAGCATGTGAAAGTGAATTGAATGAAGTTACTGGTACAAAGATTGCTTATGAAACA	1859
Qy	1017	AAAATGGACCTGGTTCAAACCTTCAGAAGCTGTGCAGGAGTCACTTTACCCTGTAACACAG	1076
Db	1860	AAAATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCACAG	1919
Qy	1077	CTTTGCCCATCTTTTGAAGAATCTGAAGCTACTCCGTCACCGGTTTTGCCTGACATTGTC	1136
Db	1920	CTTTGCCCATCATTTGAAGAGTCAGAAGCTACTCCTTCACCAGTTTTGCCTGACATTGTT	1979
Qy	1137	ATGGAAGCACCATTAAATTCTGTAGTTCCTAGTGCTGGTGCTTCTGCAGTGCAGCTCAGT	1196
Db	1980	ATGGAAGCACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGATACAGCCCAGC	2039
Qy	1197	TCATCACCATTAGAACTCTTCCTTCAGTTAATTATGAAAGCATAAAGTTTGAGCCTGAA	1256
Db	2040	TCATCACCATTAGAAGC---TTCTTCAGTTAATTATGAAAGCATAAAACATGAGCCTGAA	2096
Qy	1257	AATCCCCCACCATATGAGGAGGCCATGAATGTATCACTAAAAAAGAATCAGGAATGAAT	1316
Db	2097	AACCCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAGTATCAGGAATAAAG	2156
Qy	1317	GAAGAAATCACAGAGCCTGAAGGTATTAGTGTAGCTGTTTCAGGAAACAGAAGCTCCTTAT	1376
Db	2157	GAAGAAATTAAAGAGCCTGAAAATATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTAT	2216
Qy	1377	ATATCTATTGCATGTGATTTAATTAAAGAAACAAAGATCTCTACTGAACCGACTCCAGAT	1436
Db	2217	ATATCTATTGCATGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAACCAGCTCCGGAT	2276
Qy	1437	TTCTCTAGTTATTCAGAAATAGCAGAAGTTGCACAGCCAGTGCCCCGAGCATTCTGAGCTA	1496
Db	2277	TTCTCTGATTATTCAGAAATGGCAAAAGTTGAACAGCCAGTGCCCTGATCATTCTGAGCTA	2336
Qy	1497	GTTGAAGATTCTCCCCGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCC	1556
Db	2337	GTTGAAGATTCTCACCTGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCT	2396
Qy	1557	GAAGTTCCACAAAAACAAGATGAAGCTGTAATACTTGTGAAAGAAAACCTCACTGAAATT	1616
Db	2397	GACGTTCCACAAAAACAAGATGAAACTGTGATGCTTGTGAAAGAAAGTCTCACTGAGACT	2456
Qy	1617	TCATCTGAGTCAATGACAGGACATGACAATAAGGGAAAACTCAGTGCTTCACCATCACCT	1676

Db	2457	TCATTTGAGTCAATGATAGAATATGAAAAATAAGGAAAAAACTCAGTGCTTTTGC---	CACCT	2513
Qy	1677	GAGGGAGGAAAACCGTATTTGGAGTCTTTTCAGCCCAGTTTAGGCATCACAAAAGATAACC		1736
Db	2514	GAGGGAGGAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATAACC		2573
Qy	1737	TTAGCACCTGATGAAGTTTCAGCATTGACCCAAAAGGAGAAAATCCCTTTGCAGATGGAG		1796
Db	2574	CTGTTACCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAATTCCTTTGCAGATGGAG		2633
Qy	1797	GAGCTCAATACTGCAGTTTATTCAAGTGATGGCTTATTCATTGCTCAGGAAGCAAACCTA		1856
Db	2634	GAGCTCAGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGATA		2693
Qy	1857	AGAGAAAGTGAAACATTTTCAGATTTCATCTCCGATTGAGATTATAGATGAGTTCCCGACC		1916
Db	2694	AGAGAAACTGAAACGTTTTTCAGATTTCATCTCCAATTGAAATTATAGATGAGTTCCCTACA		2753
Qy	1917	TTTGTCAGTTCTAAAGCAGATTCTTCTCTACATTAGCCAGGGAATACACTGACCTAGAA		1976
Db	2754	TTGATCAGTTCTAAAACGATTTCATTTCTAAATTAGCCAGGGAATATACTGACCTAGAA		2813
Qy	1977	GTAGCCACAAAAGTGAAATTGCTGACATCCAGGATGGAGCTGGGTTCATTGGCTTGTGCA		2036
Db	2814	GTATCCACAAAAGTGAAATTGCTAATGCCCCGGATGGAGCTGGGTTCATTGCCTTGCACA		2873
Qy	2037	GGATTGCCCCATGACCTTTCTTTCAAGAGTATACAACC-----TAAAGAGGAAGTTCAT		2090
Db	2874	GAATTGCCCCATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCAGT		2933
Qy	2091	GTCCCGATGAGTTCTCCAAAGATAGGGGTGATGTTTCAAAGGTGCCCGTACTGCCTCCA		2150
Db	2934	TTCTCAGATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCA		2993
Qy	2151	GATGTTTCTGCTTTGGATGCTCAAGCAGAGATAGGCAGCATAGAAAAACCCAAAGTTCTT		2210
Db	2994	GATGTTTCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTT		3053
Qy	2211	GTGAAAGAAGCCGAGAGAAAACCTCCTTCTGATACAGAAAAAGAGCGAAGATCTCCATCT		2270
Db	3054	GTGAAAGAAGCTGAGAAAAACCTCCTTCCGATACAGAAAAAGAGACAGATCACCATCT		3113
Qy	2271	GCTATATTTTCAGCAGAGCTGAGTAAAACCTCAGTTGTTGACCTCCTCTACTGGAGAGAC		2330
Db	3114	GCTATATTTTCAGCAGAGCTGAGTAAAACCTCAGTTGTTGACCTCCTGTACTGGAGAGAC		3173
Qy	2331	ATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCTTGTTTCCTGCTGCTCTCGCTGACAGTA		2390
Db	3174	ATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCCTATTTCCTGCTGCTTTTCATTGACAGTA		3233
Qy	2391	TTCAGCATTGTGAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCTGTGACTATCAGC		2450
Db	3234	TTCAGCATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGC		3293
Qy	2451	TTTAGGATATATAAGGGTGTGATCCAGGCTATCCAGAAATCTGATGAAGGCCACCCATTC		2510
Db	3294	TTTAGGATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTC		3353


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; APPLICANT: Twine, Natalie C.
; APPLICANT: Dorner, Andrew J.
; APPLICANT: Trepicchio, William L.
; APPLICANT: Slonim, Donna K.
; APPLICANT: Stover, Jennifer A.
; TITLE OF INVENTION: METHODS FOR DIAGNOSING RCC AND OTHER SOLID TUMORS
; FILE REFERENCE: AM101080L
; CURRENT APPLICATION NUMBER: US/10/717,597
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: US 60/459,782
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: US 60/427,982
; PRIOR FILING DATE: 2002-11-21
; NUMBER OF SEQ ID NOS: 4904
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 310
; LENGTH: 4053
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-717-597-310

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Qy	481	AAAGATACTTACAAGCAAGATAGTGATGTTTTGATTGCTGGAGGTAATATAGAGAGCAAA	540
Db	1323	AAAGATAGT---AAGGAAGATAGTGATATGTTGGCTGCTGGAGGTAATATAGAGAGCAAC	1379
Qy	541	TTGGAAGGTAAAGTGGATAAGAAACACTTTTCAGATAGCCTTGAACAAACAAATCGTGAA	600
Db	1380	TTGGAAAGTAAAGTGGATAAAAAATGTTTTGCAGATAGCCTTGAGCAAATAATCACGAA	1439
Qy	601	AAAGATAGTGAAAGCAGTAATGATGACACTTCATTTCACAGTACACCAGAAGCTGTAAGA	660
Db	1440	AAAGATAGTGAGAGTAGTAATGATGATACTTCTTTCACAGTACGCCAGAAGGTATAAAG	1499
Qy	661	GGTGGTTCCGGAGCGTACATCACGTGTGCTCCCTTTAACC---CAACAACAGAGAATGTT	717
Db	1500	GATCGTTCAGGAGCATATATCACATGTGCTCCCTTTAACCCAGCAGCAACTGAGAGCATT	1559
Qy	718	TCAACAAACATTTTTCCCTTGTTGGAAGATCATACTTCGAAAATAAGACAGATGAAAAA	777
Db	1560	GCAACAAACATTTTTCTTTGTTAGGAGATCCTACTTCAGAAAATAAGACCGATGAAAAA	1619
Qy	778	AAGATAGAA-AAAAAAGGCACAAATTGTAACAGAGAAGAATGCAAGTGTCAAGACATCA	836
Db	1620	AAAATAGAAGAAAAGAAGGCCAAATAGTAACAGAGAAGAATACTAGCACCAAACATCA	1679
Qy	837	AACCCTTTCTTATGGCAGCACAGGAGTCTAAGACAGATTACGTTACAACAGATCATGTG	896
Db	1680	AACCCTTTCTTGTAGCAGCACAGGATTCTGAGACAGATTATGTACAAACAGATAATTTA	1739
Qy	897	TCAAAGGTGACCGAGGAAGTAGTGGCAAACATGCCTGAAGGTCTAACCCAGATTTGGTT	956
Db	1740	ACAAAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCCAGATTTAGTA	1799
Qy	957	CAGGAAGCATGTGAAAGTGAATTGAATGAAGCTACTGGTACAAAAATTGCCTTTGAAACA	1016
Db	1800	CAGGAAGCATGTGAAAGTGAATTGAATGAAGTTACTGGTACAAAGATTGCTTATGAAACA	1859
Qy	1017	AAAATGGACCTGGTTCAAACCTCAGAAGCTGTGCAGGAGTCACTTTACCCTGTAACACAG	1076
Db	1860	AAAATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCACAG	1919
Qy	1077	CTTTGCCCATCTTTTGAAGAATCTGAAGCTACTCCGTCACCGGTTTTGCCTGACATTGTC	1136
Db	1920	CTTTGCCCATCATTTGAAGAGTCAGAAGCTACTCCTTCACCAGTTTTGCCTGACATTGTT	1979
Qy	1137	ATGGAAGCACCATTAAATTCTGTAGTTCCTAGTGCTGGTGCTTCTGCAGTGCAGCTCAGT	1196
Db	1980	ATGGAAGCACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGATACAGCCCAGC	2039
Qy	1197	TCATCACCATTAGAACTCTTCCTTCAGTTAATTATGAAAGCATAAAGTTTGAGCCTGAA	1256
Db	2040	TCATCACCATTAGAAGC---TTCTTCAGTTAATTATGAAAGCATAAAACATGAGCCTGAA	2096
Qy	1257	AATCCCCCACCATATGAGGAGGCCATGAATGTATCACTAAAAAAGAATCAGGAATGAAT	1316
Db	2097	AACCCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAGTATCAGGAATAAAG	2156
Qy	1317	GAAGAAATCACAGAGCCTGAAGGTATTAGTGTAGCTGTTGAGGAAACAGAAGCTCCTTAT	1376

Db	2157	GAAGAAATTAAAGAGCCTGAAAAATATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTAT	2216
Qy	1377	ATATCTATTGCATGTGATTTAATTAAAGAAACAAAGATCTCTACTGAACCGACTCCAGAT	1436
Db	2217	ATATCTATTGCATGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAACCGACTCCGGAT	2276
Qy	1437	TTCTCTAGTTATTTCAGAAATAGCAGAAGTTGCACAGCCAGTGCCCGAGCATTCTGAGCTA	1496
Db	2277	TTCTCTGATTATTTCAGAAATGGCAAAAGTTGAACAGCCAGTGCCTGATCATTCTGAGCTA	2336
Qy	1497	GTTGAAGATTCCCTCCCCGATTCTGAACCGATTGACTTATTTAGTGATGATTCAATACCC	1556
Db	2337	GTTGAAGATTCCCTCACCTGATTCTGAACCGATTGACTTATTTAGTGATGATTCAATACCT	2396
Qy	1557	GAAGTTCCACAAAAACAAGATGAAGCTGTAATACTTGTGAAAGAAAACCTCACTGAAATT	1616
Db	2397	GACGTTCCACAAAAACAAGATGAAACTGTGATGCTTGTGAAAGAAAAGTCTCACTGAGACT	2456
Qy	1617	TCATCTGAGTCAATGACAGGACATGACAATAAGGGAAAACTCAGTGCTTCACCATCACCT	1676
Db	2457	TCATTTGAGTCAATGATAGAATATGAAAAATAAGGAAAAAACTCAGTGCTTTGC---CACCT	2513
Qy	1677	GAGGGAGGAAAACCGTATTTGGAGTCTTTTCAGCCCAGTTTAGGCATCACAAAAGATACC	1736
Db	2514	GAGGGAGGAAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATACC	2573
Qy	1737	TTAGCACCTGATGAAGTTTCAGCATTGACCCAAAAGGAGAAAAATCCCTTTGCAGATGGAG	1796
Db	2574	CTGTTACCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAAATTCCTTTGCAGATGGAG	2633
Qy	1797	GAGCTCAATACTGCAGTTTATTCAAGTGATGGCTTATTCATTGCTCAGGAAGCAAACCTA	1856
Db	2634	GAGCTCAGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGATA	2693
Qy	1857	AGAGAAAGTGAAACATTTTCAGATTTCATCTCCGATTGAGATTATAGATGAGTTCCCGACC	1916
Db	2694	AGAGAAACTGAAACGTTTTCAGATTTCATCTCCAATTGAAATTATAGATGAGTTCCCTACA	2753
Qy	1917	TTTGTCAGTTCTAAAGCAGATTCTTCTCCTACATTAGCCAGGGAATACACTGACCTAGAA	1976
Db	2754	TTGATCAGTTCTAAAACTGATTCAATTTCTAAATTAGCCAGGGAATATACTGACCTAGAA	2813
Qy	1977	GTAGCCACAAAAAGTGAAATTGCTGACATCCAGGATGGAGCTGGGTTCATTGGCTTGTGCA	2036
Db	2814	GTATCCACAAAAAGTGAAATTGCTAATGCCCCGGATGGAGCTGGGTTCATTGCCTTGACA	2873
Qy	2037	GGATTGCCCCATGACCTTTCTTTCAAGAGTATACAACC-----TAAAGAGGAAGTTCAT	2090
Db	2874	GAATTGCCCCATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCAGT	2933
Qy	2091	GTCCCAGATGAGTTCTCCAAAGATAGGGGTGATGTTTCAAAGGTGCCCCGTA CTGCCTCCA	2150
Db	2934	TTCTCAGATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCA	2993
Qy	2151	GATGTTTCTGCTTTGGATGCTCAAGCAGAGATAGGCAGCATAGAAAAACCCAAAGTTCTT	2210

Db 2994 GATGTTTCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTT 3053
 Qy 2211 GTGAAAGAAGCCGAGAGAAAACTTCCTTCTGATACAGAAAAAGAGCGAAGATCTCCATCT 2270
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 Db 3054 GTGAAAGAAGCTGAGAAAAAACTTCCTTCCGATACAGAAAAAGAGGACAGATCACCATCT 3113
 Qy 2271 GCTATATTTTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGAC 2330
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 Db 3114 GCTATATTTTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTGTACTGGAGAGAC 3173
 Qy 2331 ATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCTTGTTTCCTGCTGCTCTCGCTGACAGTA 2390
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 Db 3174 ATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCCTATTCCTGCTGCTTTTCATTGACAGTA 3233
 Qy 2391 TTCAGCATTGTGAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCTGTGACTATCAGC 2450
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 Db 3234 TTCAGCATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGC 3293
 Qy 2451 TTTAGGATATATAAGGGTGTGATCCAGGCTATCCAGAAATCTGATGAAGGCCACCCATTC 2510
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 Db 3294 TTTAGGATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTC 3353
 Qy 2511 AGGGCATATTTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGCAAT 2570
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 Db 3354 AGGGCATATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGTAAT 3413
 Qy 2571 TCTGCTCTTGGTCATGTAACTGCACAATAAAAGAACTCAGACGCCTCTTCTTAGTTGAT 2630
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 Db 3414 TCTGCTCTTGGTCATGTGAAGTGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGAT 3473
 Qy 2631 GATTTAGTTGATTCTCTGAAGTTTGAGTGTGATGTGGGTATTTACCTATGTTGGTGCC 2690
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 Db 3474 GATTTAGTTGATTCTCTGAAGTTTGAGTGTGATGTGGGTATTTACCTATGTTGGTGCC 3533
 Qy 2691 TTGTTCAATGGTCTGACACTACTAATTTTGGCTCTGATTTCACTCTTCAGTGTTCTTGTT 2750
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 Db 3534 TTGTTAATGGTCTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTTCTTGTT 3593
 Qy 2751 ATTTATGAACGGCATCAGGCGCAAATAGATCATTATCTGGGACTTGCAAATAAGAATGTT 2810
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 Db 3594 ATTTATGAACGGCATCAGGCACAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTT 3653
 Qy 2811 AAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGAATGA 2870
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 Db 3654 AAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGAATGA 3713
 Qy 2871 GAAAGCCTGAAAGAGTTAACAATAGAGGAGTTTATCTTTAAAGGGGATATTCATTTGATT 2930
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 Db 3714 AAACGCCCAAATAATTA-----GTAGGAGTTCATCTTTAAAGGGGATATTCATTTGATT 3768
 Qy 2931 CCATTGGGGAGGGTCAGGGAAGAACAAGCCTTGACATTGCAGTGCAGTTTCAC----- 2984
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 Db 3769 ATACGGGGGAGGGTCAGGGAAGAACGAA-CCTTGACGTTGCAGTGCAGTTTCACAGATCG 3827
 Qy 2985 -----AGATCTTTATTTTGTAGCAACGCAGTG-TCTGAGGAAAAATGACCTGTCTTGACTG 3038
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 Db 3828 TTGTTAGATCTTTATTTTGTAGCCATGCACTGTTGTGAGGAAAAATTACCTGTCTTGACTG 3887

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Qy      3039 CCCTGTGTTTCATCATCTTAAGTATTGTAAGCTGCTATGTATGGATTTAAATCGTAATCAT 3098
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Db      3888 CCATGTGTTTCATCATCTTAAGTATTGTAAGCTGCTATGTATGGATTTAAACCGTAATCAT 3947

Qy      3099 ATTTGTTTTTCCTGTATGAGGCACTGGTGAATAAACAAAGATCTGAGAAAGCTGTATATT 3158
          | | ||||| | ||||| | | ||| |||||
Db      3948 A--TCTTTTCCTATCTGAGGCACTGGTGGA-----ATAAAAAACCTGTATATT 3994

Qy      3159 ACACTTTGTGCGCAGGTAGTCTTGCTGTAT-TTGGGGAATTGCAAAGAAAGTGGAGCT 3214
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Db      3995 TTACTTTGTTGCAGATAGTCTTGCCGCATCTTGGCAAGTTGCAGAGATGGTGGAGCT 4051

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RESULT 5

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US-09-789-386-1
; Sequence 1, Application US/09789386
; Patent No. US20020010324A1
; GENERAL INFORMATION:
; APPLICANT: MICHALOVICH, DAVID
; APPLICANT: PRINJHA, RABINDER KUMAR
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP-30165-C1
; CURRENT APPLICATION NUMBER: US/09/789,386
; CURRENT FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: U.K. 9916898.1
; PRIOR FILING DATE: 1999-07-19
; PRIOR APPLICATION NUMBER: U.K. 9816024.5
; PRIOR FILING DATE: 1998-07-22
; PRIOR APPLICATION NUMBER: US 09/359,208
; PRIOR FILING DATE: 1999-07-22
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 3579
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
US-09-789-386-1

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Query Match          58.0%; Score 2223.6; DB 9; Length 3579;
Best Local Similarity 87.5%; Pred. No. 0;
Matches 2519; Conservative 0; Mismatches 339; Indels 22; Gaps 7;

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Qy      1 CTATCTCCTCTCTCAGCCGCTGCTTTTTAAAGAACGTGAATACCTTGGTGATTTACCAGCA 60
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Db      712 CTGTCTCCTCTCTCAGCCGCTTCTTTCAAAGAACATGAATACCTTGGAATTTGTCAACA 771

Qy      61 GTACTGCCCCACTGAAGGAACACTTCCAGCAACTTCAAATGAAGCTTCTAAAGCATTCTCA 120
          ||| | ||||| ||||| || || | | ||||| |||||
Db      772 GTATTACCCACTGAAGGAACACTTCAAGAAAATGTCAGTGAAGCTTCTAAAGAGGTCTCA 831

Qy      121 GAGAAGGCCAAAAAATCCATTTGTAGAGAGAAATTTAACAGAATTTTCAGAATTGGAATAT 180
          ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      832 GAGAAGGCCAAAACTCTACTCATAGATAGAGATTTAACAGAGTTTTTCAGAATTAGAATAC 891

Qy      181 TCAGAAATGGAATCATCATTAGTGGCTCTCAAAAGGCAGAACCTGCCGTAACAGTAGCG 240
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Db	892	TCAGAAATGGGATCATCGTTTCAGTGTCTCTCCAAAAGCAGAATCTGCCGTAATAGTAGCA	951
Qy	241	AATCCTAGGGACGAAATAGTTGTGAGGAGTAGAGATAAAGAAGAGGACTTAGTTAGTCTT	300
Db	952	AATCCTAGGGAAGAAATAATCGTGAAAAATAAAGATGAAGAAGAGAAGTTAGTTAGTAAT	1011
Qy	301	AACATCCTTCATACTCAGCAGGAGTTATCTACAGTCCTTACGAAATCAGTTGAAGAAGAA	360
Db	1012	AACATCCTTCATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGGTTAAAGAGGAT	1071
Qy	361	GATAGAGTTCTGTCTCCAGAAAAACAAAGGACAGTTTTAAGGAAAAGGGAGTTGCAGCA	420
Db	1072	GA---AGTTGTGTCTTCAGAAAAAGCAAAGACAGTTTTAATGAAAAGAGAGTTGCAGTG	1128
Qy	421	GAAGCTTCTATGGGGGAGGAATATGCAGACTTCAAACCATTGAGCGAGTATGGGAAGTG	480
Db	1129	GAAGCTCCTATGAGGGAGGAATATGCAGACTTCAAACCATTGAGCGAGTATGGGAAGTG	1188
Qy	481	AAAGATACTTACAAGCAAGATAGTGATGTTTTGATTGCTGGAGGTAATATAGAGAGCAAA	540
Db	1189	AAAGATAGT---AAGGAAGATAGTGATATGTTGGTGCTGGAGGTAATAATCGAGAGCAAC	1245
Qy	541	TTGGAAGGTAAAGTGGATAAGAAACACTTTTCAGATAGCCTTGAACAAACAAATCGTGAA	600
Db	1246	TTGGAAGGTAAAGTGGATAAAAAATGTTTTGCAGATAGCCTTGAACAACTAATCACGAA	1305
Qy	601	AAAGATAGTGAAAGCAGTAATGATGACACTTCATTTCCCAGTACACCAGAAGCTGTAAGA	660
Db	1306	AAAGATAGTGAGAGTAGTAATGATGATACTTCTTTCCCCAGTACGCCAGAAGGTATAAAG	1365
Qy	661	GGTGGTTCCGGAGCGTACATCACGTGTGCTCCCTTTAACC---CAACAAGTGAAGTGT	717
Db	1366	GATCGTCCAGGAGCATATATCACATGTGCTCCCTTTAACCCAGCAGCAACTGAGAGCATT	1425
Qy	718	TCAACAAACATTTTTCCCTTGTTGGAAGATCATACTTCGGAAAATAAGACAGATGAAAAA	777
Db	1426	GCAACAAACATTTTTCTTTGTTAGGAGATCCTACTTCAGAAAATAAGACCGATGAAAAA	1485
Qy	778	AAGATAGAA-AAAAAAGGCACAAATTGTAACAGAGAAGAATGCAAGTGTCAAGACATCA	836
Db	1486	AAAATAGAAGAAAAGAAGGCCCAAATAGTAACAGAGAAGAATACTAGCACCAAACATCA	1545
Qy	837	AACCCTTTCTTATGGCAGCACAGGAGTCTAAGACAGATTACGTTACAACAGATCATGTG	896
Db	1546	AACCCTTTTCTTGTAGCAGCACAGGATTCTGAGACAGATTATGTCACAACAGATAATTTA	1605
Qy	897	TCAAAGGTGACCGAGGAAGTAGTGGCAAACATGCCTGAAGGTCTAACCCAGATTTGGTT	956
Db	1606	ACAAAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCCAGATTTAGTA	1665
Qy	957	CAGGAAGCATGTGAAAGTGAATTGAATGAAGCTACTGGTACAAAATTGCCTTTGAAACA	1016
Db	1666	CAGGAAGCATGTGAAAGTGAATTGAATGAAGTTACTGGTACAAAGATTGCTTATGAAACA	1725
Qy	1017	AAAATGGACCTGGTTCAAACTTCAGAAGCTGTGCAGGAGTCACTTTACCCTGTAACACAG	1076
Db	1726	AAAATGGACTTGTTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCACAG	1785

Qy	1077	CTTTGCCCATCTTTTGAAGAATCTGAAGCTACTCCGTCACCGGTTTTGCCTGACATTGTC	1136
Db	1786	CTTTGCCCATCATTTGAAGAGTCAGAAGCTACTCCTTCACCAGTTTTGCCTGACATTGTT	1845
Qy	1137	ATGGAAGCACCATTAAATTCTGTAGTTCCTAGTGCTGGTGCTTCTGCAGTGCAGCTCAGT	1196
Db	1846	ATGGAAGCACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGATACAGCCCAGC	1905
Qy	1197	TCATCACCATTAGAAACTCTTCCTTCAGTTAATTATGAAAGCATAAAGTTTGAGCCTGAA	1256
Db	1906	TCATCACCATTAGAAGC---TTCTTCAGTTAATTATGAAAGCATAAAACATGAGCCTGAA	1962
Qy	1257	AATCCCCCACCATATGAGGAGGCCATGAATGTATCACTAAAAAAGAATCAGGAATGAAT	1316
Db	1963	AACCCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAGTATCAGGAATAAAG	2022
Qy	1317	GAAGAAATCACAGAGCCTGAAGGTATTAGTGTAGCTGTTTCAGGAAACAGAAGCTCCTTAT	1376
Db	2023	GAAGAAATTAAAGAGCCTGAAATATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTAT	2082
Qy	1377	ATATCTATTGCATGTGATTTAATTAAAGAAACAAAGATCTCTACTGAACCGACTCCAGAT	1436
Db	2083	ATATCTATTGCATGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAACCAGCTCCGGAT	2142
Qy	1437	TTCTCTAGTTATTCAGAAATAGCAGAAGTTGCACAGCCAGTGCCCCGAGCATTCTGAGCTA	1496
Db	2143	TTCTCTGATTATTCAGAAATGGCAAAAGTTGAACAGCCAGTGCCTGATCATTCTGAGCTA	2202
Qy	1497	GTTGAAGATTCCCTCCCCGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCC	1556
Db	2203	GTTGAAGATTCCCTCACCTGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCT	2262
Qy	1557	GAAGTTCCACAAAAACAAGATGAAGCTGTAATACTTGTGAAAGAAAACCTCACTGAAATT	1616
Db	2263	GACGTTCCACAAAAACAAGATGAAACTGTGATGCTTGTGAAAGAAAGTCTCACTGAGACT	2322
Qy	1617	TCATCTGAGTCAATGACAGGACATGACAATAAGGGAAAACCTCAGTGCTTCACCATCACCT	1676
Db	2323	TCATTTGAGTCAATGATAGAATATGAAAATAAGGAAAAACTCAGTGCTTTGC---CACCT	2379
Qy	1677	GAGGGAGGAAAACCGTATTTGGAGTCTTTTCAGCCCAGTTTAGGCATCACAAAAGATACC	1736
Db	2380	GAGGGAGGAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATACC	2439
Qy	1737	TTAGCACCTGATGAAGTTTTCAGCATTGACCCAAAAGGAGAAAATCCCTTTGCAGATGGAG	1796
Db	2440	CTGTTACCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAATTCCTTTGCAGATGGAG	2499
Qy	1797	GAGCTCAATACTGCAGTTTATTCAAGTGATGGCTTATTCATTGCTCAGGAAGCAAACCTA	1856
Db	2500	GAGCTCAGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGATA	2559
Qy	1857	AGAGAAAGTGAAACATTTTCAGATTCTCTCCGATTGAGATTATAGATGAGTTCCCGACC	1916
Db	2560	AGAGAAACTGAAACGTTTTTCAGATTCTCTCCAATTGAAATTATAGATGAGTTCCCTACA	2619

Qy	1917	TTTGTCAAGTTCTAAAGCAGATTCTTCTCCTACATTAGCCAGGGGAATACACTGACCTAGAA	1976
Db	2620	TTGATCAGTTCTAAAACTGATTCATTTTCTAAATTAGCCAGGGAATATACTGACCTAGAA	2679
Qy	1977	GTAGCCACAAAAGTGAAATTGCTGACATCCAGGATGGAGCTGGGTCATTGGCTTGTGCA	2036
Db	2680	GTATCCACAAAAGTGAAATTGCTAATGCCCCGATGGAGCTGGGTCATTGCCTTGCACA	2739
Qy	2037	GGATTGCCCCATGACCTTTCTTTCAAGAGTATACAACC-----TAAAGAGGAAGTTCAT	2090
Db	2740	GAATTGCCCCATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCAGT	2799
Qy	2091	GTCCAGATGAGTTCTCCAAAGATAGGGGTGATGTTTCAAAGGTGCCCGTACTGCCTCCA	2150
Db	2800	TTCTCAGATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCA	2859
Qy	2151	GATGTTTCTGCTTTGGATGCTCAAGCAGAGATAGGCAGCATAGAAAACCCAAAGTTCTT	2210
Db	2860	GATGTTTCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTT	2919
Qy	2211	GTGAAAGAAGCCGAGAGAAAACCTCCTTCTGATACAGAAAAGAGCGAAGATCTCCATCT	2270
Db	2920	GTGAAAGAAGCTGAGAAAAACCTCCTTCCGATACAGAAAAGAGGACAGATCACCATCT	2979
Qy	2271	GCTATATTTTCAGCAGAGCTGAGTAAACCTTCAGTTGTTGACCTCCTCTACTGGAGAGAC	2330
Db	2980	GCTATATTTTCAGCAGAGCTGAGTAAACCTTCAGTTGTTGACCTCCTGTACTGGAGAGAC	3039
Qy	2331	ATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCTTGTTTCTGCTGCTCTCGCTGACAGTA	2390
Db	3040	ATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCCTATTCTGCTGCTTTTCATTGACAGTA	3099
Qy	2391	TTCAGCATTGTGAGTGTAAACGGCTACATTGCCTTGGCCCTGCTCTCTGTGACTATCAGC	2450
Db	3100	TTCAGCATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGC	3159
Qy	2451	TTTAGGATATATAAGGGTGTGATCCAGGCTATCCAGAAATCTGATGAAGGCCACCCATTC	2510
Db	3160	TTTAGGATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTC	3219
Qy	2511	AGGGCATATTTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGCAAT	2570
Db	3220	AGGGCATATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTTACAAGTACAGTAAT	3279
Qy	2571	TCTGCTCTTGGTCATGTAACTGCACAATAAAAGAACTCAGACGCCTCTTCTTAGTTGAT	2630
Db	3280	TCTGCTCTTGGTCATGTGAACGACAGATAAAGGAACCTCAGGCGCCTCTTCTTAGTTGAT	3339
Qy	2631	GATTTAGTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCC	2690
Db	3340	GATTTAGTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCC	3399
Qy	2691	TTGTTCAATGGTCTGACACTACTAATTTTGGCTCTGATTTCACTCTTCAGTGTTTCTGTT	2750
Db	3400	TTGTTTAAATGGTCTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTTTCTGTT	3459
Qy	2751	ATTTATGAACGGCATCAGGCGCAAATAGATCATTATCTGGGACTTGCAAATAAGAATGTT	2810

Db 832 GAGAAGGCCAAAACTCTACTCATAGATAGAGATTTAACAGAGTTTTTCAGAATTAGAATAC 891
 Qy 181 TCAGAAATGGAATCATCATTCAGTGGCTCTCAAAGGCAGAACCTGCCGTAACAGTAGCG 240
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 892 TCAGAAATGGGATCATCGTTCAGTGTCTCTCCAAAGCAGAAATCTGCCGTAATAGTAGCA 951
 Qy 241 AATCCTAGGGACGAAATAGTTGTGAGGAGTAGAGATAAAGAAGAGGACTTAGTTAGTCTT 300
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 952 AATCCTAGGGAAGAAATAATCGTGAAAAATAAAGATGAAGAAGAGAAGTTAGTTAGTAAT 1011
 Qy 301 AACATCCTTCATACTCAGCAGGAGTTATCTACAGTCCTTACGAAATCAGTTGAAGAAGAA 360
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1012 AACATCCTTCATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGGTTAAAGAGGAT 1071
 Qy 361 GATAGAGTTCTGTCTCCAGAAAAACAAAGGACAGTTTTTAAGGAAAAGGGAGTTGCAGCA 420
 || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1072 GA---AGTTGTGTCTTCAGAAAAAGCAAAAGACAGTTTTAATGAAAAGAGAGTTGCAGTG 1128
 Qy 421 GAAGCTTCTATGGGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTG 480
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1129 GAAGCTCCTATGAGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTG 1188
 Qy 481 AAAGATACTTACAAGCAAGATAGTGATGTTTTGATTGCTGGAGGTAATATAGAGAGCAAA 540
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1189 AAAGATAGT---AAGGAAGATAGTGATATGTTGGCTGCTGGAGGTAATATCGAGAGCAAC 1245
 Qy 541 TTGGAAGGTAAAGTGGATAAGAAACACTTTTCAGATAGCCTTGAACAAACAAATCGTGAA 600
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1246 TTGGAAGGTAAAGTGGATAAAAAATGTTTTGCAGATAGCCTTGAACAACTAATCACGAA 1305
 Qy 601 AAAGATAGTGAAAGCAGTAATGATGACACTTCATTTCCAGTACACCAGAAGCTGTAAGA 660
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1306 AAAGATAGTGAGAGTAGTAATGATGATACTTCTTTCCAGTACGCCAGAAGGTATAAAG 1365
 Qy 661 GGTGGTTCCGGAGCGTACATCACGTGTGCTCCCTTTAACC---CAACAACAGAGAATGTT 717
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1366 GATCGTCCAGGAGCATATATCACATGTGCTCCCTTTAACCAGCAGCAACTGAGAGCATT 1425
 Qy 718 TCAACAAACATTTTCCCTTGTTGGAAGATCATACTTCGGAAAATAAGACAGATGAAAAA 777
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1426 GCAACAAACATTTTCCCTTGTTAGGAGATCCTACTTCAGAAAATAAGACCGATGAAAAA 1485
 Qy 778 AAGATAGAA-AAAAAAGGCACAAATTGTAACAGAGAAGAATGCAAGTGTCAAGACATCA 836
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1486 AAAATAGAAGAAAAGAAGGCCCAAATAGTAACAGAGAAGAATACTAGCACCAAAACATCA 1545
 Qy 837 AACCTTTTCTTATGGCAGCACAGGAGTCTAAGACAGATTACGTTACAACAGATCATGTG 896
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1546 AACCTTTTCTTGTAGCAGCACAGGATTCTGAGACAGATTATGTCACAACAGATAATTTA 1605
 Qy 897 TCAAAGGTGACCGAGGAAGTAGTGGCAAACATGCCTGAAGGTCTAACCCAGATTTGGTT 956
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1606 ACAAAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCCAGATTTAGTA 1665
 Qy 957 CAGGAAGCATGTGAAAGTGAATTGAATGAAGCTACTGGTACAAAATTCCTTTGAAACA 1016
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1666 CAGGAAGCATGTGAAAGTGAATTGAATGAAGTTACTGGTACAAAGATTGCTTATGAAACA 1725

Qy	1017	AAAATGGACCTGGTTCAAACCTTCAGAAGCTGTGCAGGAGTCACTTTACCCTGTAACACAG	1076
Db	1726	AAAATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCACAG	1785
Qy	1077	CTTTGCCCATCTTTTGAAGAATCTGAAGCTACTCCGTCACCGGTTTTGCCTGACATTGTC	1136
Db	1786	CTTTGCCCATCATTTGAAGAGTCAGAAGCTACTCCTTCACCAGTTTTGCCTGACATTGTT	1845
Qy	1137	ATGGAAGCACCATTAAATTCTGTAGTTCCTAGTGCTGGTGCTTCTGCAGTGCAGCTCAGT	1196
Db	1846	ATGGAAGCACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGATACAGCCCAGC	1905
Qy	1197	TCATCACCATTAGAACTCTTCCTTCAGTTAATTATGAAAGCATAAAGTTTGAGCCTGAA	1256
Db	1906	TCATCACCATTAGAAGC---TTCTTCAGTTAATTATGAAAGCATAAAACATGAGCCTGAA	1962
Qy	1257	AATCCCCCACCATATGAGGAGGCCATGAATGTATCACTAAAAAAGAATCAGGAATGAAT	1316
Db	1963	AACCCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAGTATCAGGAATAAAG	2022
Qy	1317	GAAGAAATCACAGAGCCTGAAGGTATTAGTGTAGCTGTTCAGGAAACAGAAGCTCCTTAT	1376
Db	2023	GAAGAAATTAAAGAGCCTGAAAATATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTAT	2082
Qy	1377	ATATCTATTGCATGTGATTTAATTAAAGAAACAAAGATCTCTACTGAACCGACTCCAGAT	1436
Db	2083	ATATCTATTGCATGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAACCAGCTCCGGAT	2142
Qy	1437	TTCTCTAGTTATTCAGAAATAGCAGAAAGTTGCACAGCCAGTGCCCCGAGCATTCTGAGCTA	1496
Db	2143	TTCTCTGATTATTCAGAAATGGCAAAAGTTGAACAGCCAGTGCCTGATCATTCTGAGCTA	2202
Qy	1497	GTTGAAGATTCCCTCCCCGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCC	1556
Db	2203	GTTGAAGATTCCCTCACCTGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCT	2262
Qy	1557	GAAGTTCACAAAAACAAGATGAAGCTGTAATACTTGTGAAAGAAAACCTCACTGAAATT	1616
Db	2263	GACGTTCCACAAAAACAAGATGAAACTGTGATGCTTGTGAAAGAAAGTCTCACTGAGACT	2322
Qy	1617	TCATCTGAGTCAATGACAGGACATGACAATAAGGGAAAACCTCAGTGCTTCACCATCACCT	1676
Db	2323	TCATTTGAGTCAATGATAGAATATGAAAATAAGGAAAAACTCAGTGCTTTGC---CACCT	2379
Qy	1677	GAGGGAGGAAAACCGTATTTGGAGTCTTTTCAGCCAGTTTAGGCATCACAAAAGATACC	1736
Db	2380	GAGGGAGGAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATACC	2439
Qy	1737	TTAGCACCTGATGAAGTTTCAGCATTGACCCAAAAGGAGAAAATCCCTTTGCAGATGGAG	1796
Db	2440	CTGTTACCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAATTCCTTTGCAGATGGAG	2499
Qy	1797	GAGCTCAATACTGCAGTTTATTCAAGTGATGGCTTATTCATTGCTCAGGAAGCAAACCTA	1856
Db	2500	GAGCTCAGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGATA	2559

Qy	1857	AGAGAAAAGTGAAACATTTTCAGATTTCATCTCCGATTGAGATTATAGATGAGTTCCCGACC	1916
Db	2560	AGAGAAACTGAAACGTTTTCAGATTTCATCTCCAATTGAAATTATAGATGAGTTCCCTACA	2619
Qy	1917	TTTGTCTAGTTCTAAAGCAGATTCTTCTCCTACATTAGCCAGGGAATACACTGACCTAGAA	1976
Db	2620	TTGATCAGTTCTAAAAGTATTTCATTTTCTAAATTAGCCAGGGAATATACTGACCTAGAA	2679
Qy	1977	GTAGCCACACAAAAGTGAAATTGCTGACATCCAGGATGGAGCTGGGTCATTGGCTTGTGCA	2036
Db	2680	GTATCCACACAAAAGTGAAATTGCTAATGCCCCGGATGGAGCTGGGTCATTGCCTTGCACA	2739
Qy	2037	GGATTGCCCCATGACCTTTCTTTCAAGAGTATACAACC-----TAAAGAGGAAGTTCAT	2090
Db	2740	GAATTGCCCCATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCAGT	2799
Qy	2091	GTCCCAGATGAGTTCTCCAAAGATAGGGGTGATGTTTCAAAGGTGCCCGTACTGCCTCCA	2150
Db	2800	TTCTCAGATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCA	2859
Qy	2151	GATGTTTCTGCTTTGGATGCTCAAGCAGAGATAGGCAGCATAGAAAAACCCAAAGTTCTT	2210
Db	2860	GATGTTTCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTT	2919
Qy	2211	GTGAAAGAAGCCGAGAGAAAACTTCCTTCTGATACAGAAAAAGAGCGAAGATCTCCATCT	2270
Db	2920	GTGAAAGAAGCTGAGAAAAAACTTCCTTCCGATACAGAAAAAGAGGACAGATCACCATCT	2979
Qy	2271	GCTATATTTTTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGAC	2330
Db	2980	GCTATATTTTTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTGTACTGGAGAGAC	3039
Qy	2331	ATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCTTGTTCTGCTGCTCTCGCTGACAGTA	2390
Db	3040	ATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCTTATTCCTGCTGCTTTCATTGACAGTA	3099
Qy	2391	TTCAGCATTTGTGAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCTGTGACTATCAGC	2450
Db	3100	TTCAGCATTTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGC	3159
Qy	2451	TTTAGGATATATAAGGGTGTGATCCAGGCTATCCAGAAATCTGATGAAGGCCACCCATTC	2510
Db	3160	TTTAGGATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTC	3219
Qy	2511	AGGGCATATTTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGCAAT	2570
Db	3220	AGGGCATATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGTAAT	3279
Qy	2571	TCTGCTCTTGGTCATGTGTAAGTGCACAATAAAGAACTCAGACGCCTCTTCTTAGTTGAT	2630
Db	3280	TCTGCTCTTGGTCATGTGAACTGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGAT	3339
Qy	2631	GATTTAGTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCC	2690
Db	3340	GATTTAGTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCC	3399
Qy	2691	TTGTTCAATGGTCTGACACTACTAATTTTGGCTCTGATTTCACTCTTCAGTGTTCTGTGTT	2750

Db	1012	AACATCCTTCATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGGTTAAAGAGGAT	1071
Qy	361	GATAGAGTTCTGTCTCCAGAAAAACAAAGGACAGTTTAAAGGAAAAGGGAGTTGCAGCA	420
Db	1072	GA---AGTTGTGTCTTCAGAAAAGCAAAAGACAGTTTAAATGAAAAGAGAGTTGCAGTG	1128
Qy	421	GAAGCTTCTATGGGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTG	480
Db	1129	GAAGCTCCTATGAGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTG	1188
Qy	481	AAAGATACTTACAAGCAAGATAGTGATGTTTTGATTGCTGGAGGTAATATAGAGAGCAAA	540
Db	1189	AAAGATAGT---AAGGAAGATAGTGATATGTTGGCTGCTGGAGGTAATTCGAGAGCAAC	1245
Qy	541	TTGGAAGGTAAAGTGGATAAGAAACACTTTTCAGATAGCCTTGAACAAACAAATCGTGAA	600
Db	1246	TTGGAAGGTAAAGTGGATAAAAAATGTTTTCAGATAGCCTTGAACAAACAAATCGTGAA	1305
Qy	601	AAAGATAGTGAAAGCAGTAATGATGACACTTCATTTCCAGTACACCAGAAGCTGTAAGA	660
Db	1306	AAAGATAGTGAGAGTAGTAATGATGATACCTCTTCCCCAGTACGCCAGAAGGTATAAAG	1365
Qy	661	GGTGGTTCCGGAGCGTACATCACGTGTGCTCCCTTTAACC---CAACAACAGAGAATGTT	717
Db	1366	GATCGTCCAGGAGCATATATCACATGTGCTCCCTTTAACCCAGCAGCAACTGAGAGCATT	1425
Qy	718	TCAACAAACATTTTTCCCTTGTTGGAAGATCATACTTCGGAAAATAAGACAGATGAAAAA	777
Db	1426	GCAACAAACATTTTTCCCTTGTTAGGAGATCCTACTTCAGAAAATAAGACCGATGAAAAA	1485
Qy	778	AAGATAGAA-AAAAAAGGCACAAATTGTAACAGAGAAGAATGCAAGTGTCAAGACATCA	836
Db	1486	AAAATAGAAGAAAAGAAGGCCAAATAGTAACAGAGAAGAATACTAGCACCAAAACATCA	1545
Qy	837	AACCCTTTCTTATGGCAGCACAGGAGTCTAAGACAGATTACGTTACAACAGATCATGTG	896
Db	1546	AACCCTTTCTTGTAGCAGCACAGGATTCTGAGACAGATTATGTCACAACAGATAATTTA	1605
Qy	897	TCAAAGGTGACCGAGGAAGTAGTGGCAAACATGCCTGAAGGTCTAACCCAGATTGGTT	956
Db	1606	ACAAAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCCAGATTTAGTA	1665
Qy	957	CAGGAAGCATGTGAAAGTGAATTGAATGAAGCTACTGGTACAAAATTGCCTTTGAAACA	1016
Db	1666	CAGGAAGCATGTGAAAGTGAATTGAATGAAGTACTGGTACAAAGATTGCTTATGAAACA	1725
Qy	1017	AAAATGGACCTGGTTCAAACCTCAGAAGCTGTGCAGGAGTCACTTTACCCTGTAACACAG	1076
Db	1726	AAAATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCACAG	1785
Qy	1077	CTTTGCCCATCTTTGAAGAATCTGAAGCTACTCCGTACCGGTTTTGCCTGACATTGTC	1136
Db	1786	CTTTGCCCATCATTTGAAGAGTCAGAAGCTACTCCTTCACCAGTTTTGCCTGACATTGTT	1845
Qy	1137	ATGGAAGCACCATTAAATTCTGTAGTTCCTAGTGCTGGTGCTTCTGCAGTGCAGCTCAGT	1196
Db	1846	ATGGAAGCACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGATACAGCCCAGC	1905

Qy	1197	TCATCACCATTAGAACTCTTCCTTCAGTTAATTATGAAAGCATAAAGTTTGAGCCTGAA	1256
Db	1906	TCATCACCATTAGAAGC---TTCTTCAGTTAATTATGAAAGCATAAAACATGAGCCTGAA	1962
Qy	1257	AATCCCCCACCATATGAGGAGGCCATGAATGTATCACTAAAAAAGAATCAGGAATGAAT	1316
Db	1963	AACCCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAGTATCAGGAATAAAG	2022
Qy	1317	GAAGAAATCACAGAGCCTGAAGGTATTAGTGTAGCTGTTTCAGGAAACAGAAGCTCCTTAT	1376
Db	2023	GAAGAAATTAAAGAGCCTGAAATATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTAT	2082
Qy	1377	ATATCTATTGCATGTGATTTAATTAAAGAAACAAAGATCTCTACTGAACCGACTCCAGAT	1436
Db	2083	ATATCTATTGCATGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAACCAGCTCCGGAT	2142
Qy	1437	TTCTCTAGTTATTCAGAAATAGCAGAAGTTGCACAGCCAGTGCCCGAGCATTCTGAGCTA	1496
Db	2143	TTCTCTGATTATTCAGAAATGGCAAAAGTTGAACAGCCAGTGCCTGATCATTCTGAGCTA	2202
Qy	1497	GTTGAAGATTCCCTCCCCGATTCTGAACCCAGTTGACTTATTTAGTGATGATTCAATACCC	1556
Db	2203	GTTGAAGATTCCCTCACCTGATTCTGAACCCAGTTGACTTATTTAGTGATGATTCAATACCT	2262
Qy	1557	GAAGTTCCACAAAAACAAGATGAAGCTGTAATACTTGTGAAAGAAAACCTCACTGAAATT	1616
Db	2263	GACGTTCCACAAAAACAAGATGAAACTGTGATGCTTGTGAAAGAAAGTCTCACTGAGACT	2322
Qy	1617	TCATCTGAGTCAATGACAGGACATGACAATAAGGGAAAACTCAGTGCTTCACCATCACCT	1676
Db	2323	TCATTTGAGTCAATGATAGAATATGAAAAATAAGGAAAAACTCAGTGCTTTGC---CACCT	2379
Qy	1677	GAGGGAGGAAAACCGTATTTGGAGTCTTTTCAGCCAGTTTAGGCATCACAAAAGATACC	1736
Db	2380	GAGGGAGGAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATACC	2439
Qy	1737	TTAGCACCTGATGAAGTTTCAGCATTGACCCAAAAGGAGAAAATCCCTTTGCAGATGGAG	1796
Db	2440	CTGTTACCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAATTCCTTTGCAGATGGAG	2499
Qy	1797	GAGCTCAATACTGCAGTTTATTCAAGTGATGGCTTATTCATTGCTCAGGAAGCAAACCTA	1856
Db	2500	GAGCTCAGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGATA	2559
Qy	1857	AGAGAAAAGTGAAACATTTTCAGATTTCATCTCCGATTGAGATTATAGATGAGTTCCCGACC	1916
Db	2560	AGAGAAACTGAAACGTTTTTCAGATTTCATCTCCAATTGAAATTATAGATGAGTTCCCTACA	2619
Qy	1917	TTTGTGAGTTCTAAAGCAGATTCTTCTCCTACATTAGCCAGGGAATACACTGACCTAGAA	1976
Db	2620	TTGATCAGTTCTAAAACTGATTCAATTTCTAAATTAGCCAGGGAATATACTGACCTAGAA	2679
Qy	1977	GTAGCCACAAAAGTGAAATTGCTGACATCCAGGATGGAGCTGGGTTCATTGGCTTGTGCA	2036
Db	2680	GTATCCACAAAAGTGAAATTGCTAATGCCCCGGATGGAGCTGGGTTCATTGCCTTGACACA	2739

Qy	2037	GGATTGCCCCATGACCTTTCTTTCAAGAGTATACAACC-----TAAAGAGGAAGTTTCAT	2090
Db	2740	GAATTGCCCCATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCAGT	2799
Qy	2091	GTCCCAGATGAGTTCTCCAAAGATAGGGGTGATGTTTCAAAGGTGCCCGTACTGCCTCCA	2150
Db	2800	TTCTCAGATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCA	2859
Qy	2151	GATGTTTCTGCTTTGGATGCTCAAGCAGAGATAGGCAGCATAGAAAAACCCAAAGTTCTT	2210
Db	2860	GATGTTTCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTT	2919
Qy	2211	GTGAAAGAAGCCGAGAGAAAACCTCCTTCTGATACAGAAAAAGAGCGAAGATCTCCATCT	2270
Db	2920	GTGAAAGAAGCTGAGAAAAAACTCCTTCCGATACAGAAAAAGAGGACAGATCACCATCT	2979
Qy	2271	GCTATATTTTCAGCAGAGCTGAGTAAAACCTCAGTTGTTGACCTCCTCTACTGGAGAGAC	2330
Db	2980	GCTATATTTTCAGCAGAGCTGAGTAAAACCTCAGTTGTTGACCTCCTGTACTGGAGAGAC	3039
Qy	2331	ATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCTTGTTTCTGCTGCTCTCGCTGACAGTA	2390
Db	3040	ATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCCTATTCTGCTGCTTTTATTGACAGTA	3099
Qy	2391	TTCAGCATTGTGAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCTGTGACTATCAGC	2450
Db	3100	TTCAGCATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGC	3159
Qy	2451	TTTAGGATATATAAGGGTGTGATCCAGGCTATCCAGAAATCTGATGAAGGCCACCCATTC	2510
Db	3160	TTTAGGATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTC	3219
Qy	2511	AGGGCATATTTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGCAAT	2570
Db	3220	AGGGCATATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGTAAT	3279
Qy	2571	TCTGCTCTTGGTCATGTTAAGTGCACAATAAAAGAACTCAGACGCCTCTTCTTAGTTGAT	2630
Db	3280	TCTGCTCTTGGTCATGTGAAGTGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGAT	3339
Qy	2631	GATTTAGTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCC	2690
Db	3340	GATTTAGTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCC	3399
Qy	2691	TTGTTCAATGGTCTGACACTACTAATTTTGGCTCTGATTTCACTCTTCAGTGTTTCCTGTT	2750
Db	3400	TTGTTTAAATGGTCTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTTTCCTGTT	3459
Qy	2751	ATTTATGAACGGCATCAGGCGCAAATAGATCATTATCTGGGACTTGCAAATAAGAATGTT	2810
Db	3460	ATTTATGAACGGCATCAGGCGCAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTT	3519
Qy	2811	AAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGAATGA	2870
Db	3520	AAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGAATGA	3579

RESULT 8

US-10-327-213-8

; Sequence 8, Application US/10327213

; Publication No. US20040121341A1

; GENERAL INFORMATION:

; APPLICANT: FILBIN, MARIE T.

; APPLICANT: DOMENICONI, MARCO

; APPLICANT: CAO, ZIXUAN

; TITLE OF INVENTION: INHIBITORS OF MYELIN-ASSOCIATED GLYCOPROTEIN (MAG)

; TITLE OF INVENTION: ACTIVITY FOR REGULATING NEURAL GROWTH AND REGENERATION

; FILE REFERENCE: CUNY/003

; CURRENT APPLICATION NUMBER: US/10/327,213

; CURRENT FILING DATE: 2002-12-20

; NUMBER OF SEQ ID NOS: 43

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 8

; LENGTH: 3579

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-327-213-8

Query Match 58.0%; Score 2223.6; DB 17; Length 3579;

Best Local Similarity 87.5%; Pred. No. 0;

Matches 2519; Conservative 0; Mismatches 339; Indels 22; Gaps 7;

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Qy      1 CTATCTCCTCTCTCAGCCGCTGCTTTTAAAGAACGTGAATACCTTGGTGATTTACCAGCA 60
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Db      712 CTGTCTCCTCTCTCAGCCGCTTCTTTCAAAGAACATGAATACCTTGGTAATTTGTCAACA 771

Qy      61 GTACTGCCCCACTGAAGGAACACTTCCAGCAACTTCAAATGAAGCTTCTAAAGCATTCTCA 120
      ||| | |||||
Db      772 GTATTACCCACTGAAGGAACACTTCAAGAAAATGTCAGTGAAGCTTCTAAAGAGGTCTCA 831

Qy      121 GAGAAGGCCAAAAAATCCATTTGTAGAGAGAAATTTAACAGAATTTTCAGAATTGGAATAT 180
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Db      832 GAGAAGGCCAAAACTCTACTCATAGATAGAGATTTAACAGAGTTTTCAGAATTAGAATAC 891

Qy      181 TCAGAAATGGAATCATCATTCAGTGGCTCTCAAAAGGCAGAACCTGCCGTAACAGTAGCG 240
      |||||
Db      892 TCAGAAATGGGATCATCGTTTCAGTGTCTCTCCAAAAGCAGAAATCTGCCGTAATAGTAGCA 951

Qy      241 AATCCTAGGGACGAAATAGTTGTGAGGAGTAGAGATAAAGAAGAGGACTTAGTTAGTCTT 300
      |||||
Db      952 AATCCTAGGGAAGAAATAATCGTGAAAAATAAAGATGAAGAAGAGAAGTTAGTTAGTAAT 1011

Qy      301 AACATCCTTCATACTCAGCAGGAGTTATCTACAGTCCTTACGAAATCAGTTGAAGAAGAA 360
      |||||
Db      1012 AACATCCTTCATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGGTTAAAGAGGAT 1071

Qy      361 GATAGAGTTCTGTCTCCAGAAAAAACAAAGGACAGTTTTAAGGAAAAGGGAGTTGCAGCA 420
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Db      1072 GA---AGTTGTGTCTTCAGAAAAAGCAAAGACAGTTTTAATGAAAAGAGAGTTGCAGTG 1128

Qy      421 GAAGCTTCTATGGGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTG 480
      |||||
Db      1129 GAAGCTCCTATGAGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTG 1188

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Qy 481 AAAGATACTTACAAGCAAGATAGTGATGTTTTGATTGCTGGAGGTAATATAGAGAGCAAA 540
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 Db 1189 AAAGATAGT---AAGGAAGATAGTGATATGTTGGCTGCTGGAGGTAAAATCGAGAGCAAC 1245

Qy 541 TTGGAAGGTAAAGTGGATAAGAAACACTTTTCAGATAGCCTTGAACAAACAAATCGTGAA 600
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 Db 1246 TTGGAAGGTAAAGTGGATAAAAAATGTTTTGCAGATAGCCTTGAACAACTAATCACGAA 1305

Qy 601 AAAGATAGTGAAAGCAGTAATGATGACACTTCATTTCCAGTACACCAGAAGCTGTAAGA 660
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 Db 1306 AAAGATAGTGAGAGTAGTAATGATGATACTTCTTTCCAGTACGCCAGAAGGTATAAAG 1365

Qy 661 GGTGGTTCGGAGCGTACATCACGTGTGCTCCCTTTAACC---CAACAACTGAGAATGTT 717
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 Db 1366 GATCGTCCAGGAGCATATATCACATGTGCTCCCTTTAACCCAGCAGCAACTGAGAGCATT 1425

Qy 718 TCAACAAACATTTTCCCTTGTGGAAGATCATACTTCGGAAAATAAGACAGATGAAAAA 777
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 Db 1426 GCAACAAACATTTTCTTTGTAGGAGATCCTACTTCAGAAAATAAGACCGATGAAAAA 1485

Qy 778 AAGATAGAA-AAAAAAGGCACAAATTGTAACAGAGAAGAATGCAAGTGTCAGACATCA 836
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 Db 1486 AAAATAGAAGAAAAGAAGGCCCAAATAGTAACAGAGAAGAATACTAGCACCAAAACATCA 1545

Qy 837 AACCTTTCTTATGGCAGCACAGGAGTCTAAGACAGATTACGTTACAACAGATCATGTG 896
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 Db 1546 AACCTTTCTTGTAGCAGCACAGGATTCTGAGACAGATTATGTCACAACAGATAATTTA 1605

Qy 897 TCAAAGGTGACCGAGGAAGTAGTGGCAAACATGCCTGAAGGTCTAACCCAGATTTGGTT 956
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 Db 1606 ACAAAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCCAGATTTAGTA 1665

Qy 957 CAGGAAGCATGTGAAAGTGAATTGAATGAAGCTACTGGTACAAAATTCCTTTGAAACA 1016
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 Db 1666 CAGGAAGCATGTGAAAGTGAATTGAATGAAGTACTGGTACAAAGATTGCTTATGAAACA 1725

Qy 1017 AAAATGGACCTGGTTCAAACCTCAGAAGCTGTGCAGGAGTCACTTTACCTGTAACACAG 1076
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 Db 1726 AAAATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCACAG 1785

Qy 1077 CTTTGCCCATCTTTGAAGAATCTGAAGCTACTCCGTCACCGGTTTTGCCTGACATTGTC 1136
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 Db 1786 CTTTGCCCATCATTTGAAGAGTCAGAAGCTACTCCTTACCAGTTTTGCCTGACATTGTT 1845

Qy 1137 ATGGAAGCACCATTAAATTCTGTAGTTCCTAGTGCTGGTGCTTCTGCAGTGCAGCTCAGT 1196
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 Db 1846 ATGGAAGCACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGATACAGCCCAGC 1905

Qy 1197 TCATCACCATTAGAACTCTTCTTCAGTTAATTATGAAAGCATAAAGTTTGAGCCTGAA 1256
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 Db 1906 TCATCACCATTAGAAGC---TTCTTCAGTTAATTATGAAAGCATAAAACATGAGCCTGAA 1962

Qy 1257 AATCCCCCACCATATGAGGAGGCCATGAATGTATCACTAAAAAAGAATCAGGAATGAAT 1316
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 Db 1963 AATCCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAGTATCAGGAATAAAG 2022

Qy 1317 GAAGAAATCACAGAGCCTGAAGGTATTAGTGTAGCTGTTGAGGAAACAGAAGCTCCTTAT 1376

Db	2023	GAAGAAATTAAAGAGCCTGAAAATATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTAT	2082
Qy	1377	ATATCTATTGCATGTGATTTAATTAAAGAAACAAAGATCTCTACTGAACCGACTCCAGAT	1436
Db	2083	ATATCTATTGCATGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAACCGACTCCGGAT	2142
Qy	1437	TTCTCTAGTTATTCAGAAATAGCAGAAGTTGCACAGCCAGTGCCCCGAGCATTCTGAGCTA	1496
Db	2143	TTCTCTGATTATTCAGAAATGGCAAAAGTTGAACAGCCAGTGCCTGATCATTCTGAGCTA	2202
Qy	1497	GTTGAAGATTTCCTCCCCGATTCTGAACCGATTGACTTATTTAGTGATGATTCAATACCC	1556
Db	2203	GTTGAAGATTTCCTCACCTGATTCTGAACCGATTGACTTATTTAGTGATGATTCAATACCT	2262
Qy	1557	GAAGTTCCACAAAAACAAGATGAAGCTGTAATACTTGTGAAAGAAAACCTCACTGAAATT	1616
Db	2263	GACGTTCCACAAAAACAAGATGAAACTGTGATGCTTGTGAAAGAAAGTCTCACTGAGACT	2322
Qy	1617	TCATCTGAGTCAATGACAGGACATGACAATAAGGGAAAACCTCAGTGCTTCACCATCACCT	1676
Db	2323	TCATTTGAGTCAATGATAGAATATGAAAATAAGGAAAAACCTCAGTGCTTTGCT---CACCT	2379
Qy	1677	GAGGGAGGAAAACCGTATTTGGAGTCTTTTCAGCCCAGTTTAGGCATCACAAAAGATACC	1736
Db	2380	GAGGGAGGAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATACC	2439
Qy	1737	TTAGCACCTGATGAAGTTTCAGCATTGACCCAAAAGGAGAAAATCCCTTTGCAGATGGAG	1796
Db	2440	CTGTTACCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAATTCCTTTGCAGATGGAG	2499
Qy	1797	GAGCTCAATACTGCAGTTTATTCAAGTGATGGCTTATTCATTGCTCAGGAAGCAAACCTA	1856
Db	2500	GAGCTCAGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGATA	2559
Qy	1857	AGAGAAAGTGAAACATTTTCAGATTTCATCTCCGATTGAGATTATAGATGAGTTCCCGACC	1916
Db	2560	AGAGAAACTGAAACGTTTTCAGATTTCATCTCCAATTGAAATTATAGATGAGTTCCCTACA	2619
Qy	1917	TTTGTGAGTTCTAAAGCAGATTCTTCTCCTACATTAGCCAGGGAATACACTGACCTAGAA	1976
Db	2620	TTGATCAGTTCTAAAACTGATTCAATTTCTAAATTAGCCAGGGAATATACTGACCTAGAA	2679
Qy	1977	GTAGCCCAACAAAAGTGAAATTGCTGACATCCAGGATGGAGCTGGGTTCATTGGCTTGTGCA	2036
Db	2680	GTATCCCAACAAAAGTGAAATTGCTAATGCCCCGGATGGAGCTGGGTTCATTGCCTTGACA	2739
Qy	2037	GGATTGCCCCATGACCTTTCTTTCAAGAGTATACAACC-----TAAAGAGGAAGTTCAT	2090
Db	2740	GAATTGCCCCATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCAGT	2799
Qy	2091	GTCCCAGATGAGTTCTCCAAAGATAGGGGTGATGTTTCAAAGGTGCCCGTACTGCCTCCA	2150
Db	2800	TTCTCAGATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCA	2859
Qy	2151	GATGTTTCTGCTTTGGATGCTCAAGCAGAGATAGGCAGCATAGAAAAACCCAAAGTTCTT	2210

Db 2860 GATGTTTCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTT 2919
 Qy 2211 GTGAAAGAAGCCGAGAGAAAACTTCCTTCTGATACAGAAAAAGAGCGAAGATCTCCATCT 2270
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 Db 2920 GTGAAAGAAGCTGAGAAAAAACTTCCTTCCGATACAGAAAAAGAGGACAGATCACCATCT 2979
 Qy 2271 GCTATATTTTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGAC 2330
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 Db 2980 GCTATATTTTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTGTACTGGAGAGAC 3039
 Qy 2331 ATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCTTGTTTCCTGCTGCTCTCGCTGACAGTA 2390
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 Db 3040 ATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCCTATTCTGCTGCTTTTCATTGACAGTA 3099
 Qy 2391 TTCAGCATTGTGAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCTGTGACTATCAGC 2450
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 Db 3100 TTCAGCATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGC 3159
 Qy 2451 TTTAGGATATATAAGGGTGTGATCCAGGCTATCCAGAAATCTGATGAAGGCCACCCATTC 2510
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 Db 3160 TTTAGGATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTC 3219
 Qy 2511 AGGGCATATTTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGCAAT 2570
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 Db 3220 AGGGCATATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGTAAT 3279
 Qy 2571 TCTGCTCTTGGTCATGTTAACTGCACAATAAAAGAACTCAGACGCCTCTTCTTAGTTGAT 2630
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 Db 3280 TCTGCTCTTGGTCATGTGAAGTGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGAT 3339
 Qy 2631 GATTTAGTTGATTCTCTGAAGTTTGCAAGTTGATGTGGGTATTTACCTATGTTGGTGCC 2690
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 Db 3340 GATTTAGTTGATTCTCTGAAGTTTGCAAGTTGATGTGGGTATTTACCTATGTTGGTGCC 3399
 Qy 2691 TTGTTCAATGGTCTGACACTACTAATTTTGGCTCTGATTTCACTCTTCAGTGTTCCCTGTT 2750
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 Db 3400 TTGTTTAAATGGTCTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTTCCCTGTT 3459
 Qy 2751 ATTTATGAACGGCATCAGGCGCAAATAGATCATTATCTGGGACTTGCAAATAAGAATGTT 2810
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 Db 3460 ATTTATGAACGGCATCAGGCGCAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTT 3519
 Qy 2811 AAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGAATGA 2870
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 Db 3520 AAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCTGAATGA 3579

RESULT 9

US-10-466-258-8

; Sequence 8, Application US/10466258

; Publication No. US20040132096A1

; GENERAL INFORMATION:

; APPLICANT: GLAXO GROUP LIMITED

; TITLE OF INVENTION: ASSAY

; FILE REFERENCE: P80966 GCW

; CURRENT APPLICATION NUMBER: US/10/466,258

; CURRENT FILING DATE: 2003-07-15

; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 3579
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3579)
US-10-466-258-8

Query Match 58.0%; Score 2223.6; DB 17; Length 3579;
Best Local Similarity 87.5%; Pred. No. 0;
Matches 2519; Conservative 0; Mismatches 339; Indels 22; Gaps 7;

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Qy      1 CTATCTCCTCTCTCAGCCGCTGCTTTTAAAGAACGTGAATACCTTGGTGATTTACCAGCA 60
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Qy      61 GTACTGCCCCACTGAAGGAACACTTCCAGCAACTTCAAATGAAGCTTCTAAAGCATTCTCA 120
      ||| | |||||
Db      772 GTATTACCCACTGAAGGAACACTTCAAGAAAATGTCAGTGAAGCTTCTAAAGAGGTCTCA 831

Qy     121 GAGAAGGCCAAAAAATCCATTTGTAGAGAGAAATTTAACAGAATTTTCAGAATTGGAATAT 180
      ||||| ||| | ||||| ||| ||||| ||||| |||||
Db     832 GAGAAGGCCAAAACTCTACTCATAGATAGAGATTTAACAGAGTTTTCAGAATTAGAATAC 891

Qy     181 TCAGAAATGGAATCATCATTTCAGTGGCTCTCAAAAGGCAGAACCTGCCGTAACAGTAGCG 240
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Db     892 TCAGAAATGGGATCATCGTTTCAGTGTCTCTCCAAAAGCAGAAATCTGCCGTAATAGTAGCA 951

Qy     241 AATCCTAGGGACGAAATAGTTGTGAGGAGTAGAGATAAAGAAGAGGACTTAGTTAGTCTT 300
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db     952 AATCCTAGGGAAGAAATAATCGTGAAAAATAAAGATGAAGAAGAGAAGTTAGTTAGTAAT 1011

Qy     301 AACATCCTTCATACTCAGCAGGAGTTATCTACAGTCCTTACGAAATCAGTTGAAGAAGAA 360
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    1012 AACATCCTTCATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGGTTAAAGAGGAT 1071

Qy     361 GATAGAGTTCTGTCTCCAGAAAAACAAAGGACAGTTTTTAAGGAAAAGGGAGTTGCAGCA 420
      || ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    1072 GA---AGTTGTGTCTTCAGAAAAAGCAAAGACAGTTTTAATGAAAAGAGAGTTGCAGTG 1128

Qy     421 GAAGCTTCTATGGGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTG 480
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    1129 GAAGCTCCTATGAGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTG 1188

Qy     481 AAAGATACTTACAAGCAAGATAGTGATGTTTTGATTGCTGGAGGTAATATAGAGAGCAAA 540
      ||||| | ||| ||||| ||||| ||||| ||||| ||||| |||||
Db    1189 AAAGATAGT---AAGGAAGATAGTGATATGTTGGCTGCTGGAGGTAATTCGAGAGCAAC 1245

Qy     541 TTGGAAGGTAAAGTGGATAAGAAACACTTTTCAGATAGCCTTGAACAAACAAATCGTGAA 600
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    1246 TTGGAAGGTAAAGTGGATAAAAAATGTTTTGCAGATAGCCTTGAAGCAACTAATCACGAA 1305

Qy     601 AAAGATAGTGAAAGCAGTAATGATGACACTTCATTTCCCAGTACACCAGAAGCTGTAAGA 660
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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Db	1306	AAAGATAGTGAGAGTAGTAATGATGATACTTCTTTCCCCAGTACGCCAGAAGGTATAAAG	1365
Qy	661	GGTGGTTCCGGAGCGTACATCACGTGTGCTCCCTTTAACC---CAACAACAGAGAATGTT	717
Db	1366	GATCGTCCAGGAGCATATATCACATGTGCTCCCTTTAACCCAGCAGCAACTGAGAGCATT	1425
Qy	718	TCAACAAACATTTTTCCCTTGTTGGAAGATCATACTTCGGAAAATAAGACAGATGAAAAA	777
Db	1426	GCAACAAACATTTTTCCCTTGTTAGGAGATCCTACTTCAGAAAATAAGACCGATGAAAAA	1485
Qy	778	AAGATAGAA-AAAAAAGGCACAAATTGTAACAGAGAAGAATGCAAGTGTCAAGACATCA	836
Db	1486	AAAATAGAAGAAAAGAAGGCCCAAATAGTAACAGAGAAGAATACTAGCACCAAACATCA	1545
Qy	837	AACCCCTTTCTTATGGCAGCACAGGAGTCTAAGACAGATTACGTTACAACAGATCATGTG	896
Db	1546	AACCCCTTTCTTGTAGCAGCACAGGATTCTGAGACAGATTATGTCACAACAGATAATTTA	1605
Qy	897	TCAAAGGTGACCGAGGAAGTAGTGGCAAACATGCCTGAAGGTCTAACCCAGATTTGGTT	956
Db	1606	ACAAAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCCAGATTTAGTA	1665
Qy	957	CAGGAAGCATGTGAAAGTGAATTGAATGAAGCTACTGGTACAAAATTGCCTTTGAAACA	1016
Db	1666	CAGGAAGCATGTGAAAGTGAATTGAATGAAGTTACTGGTACAAAGATTGCTTATGAAACA	1725
Qy	1017	AAAATGGACCTGGTTCAAACCTTCAGAAGCTGTGCAGGAGTCACTTTACCCTGTAACACAG	1076
Db	1726	AAAATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCACAG	1785
Qy	1077	CTTTGCCCATCTTTTGAAGAATCTGAAGCTACTCCGTACCGGTTTTGCCTGACATTGTC	1136
Db	1786	CTTTGCCCATCATTTGAAGAGTCAGAAGCTACTCCTTCACCAAGTTTTGCCTGACATTGTT	1845
Qy	1137	ATGGAAGCACCATTAAATTCTGTAGTTCCTAGTGCTGGTGCTTCTGCAGTGCAGCTCAGT	1196
Db	1846	ATGGAAGCACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGATACAGCCCAGC	1905
Qy	1197	TCATCACCATTAGAACTCTTCCTTCAGTTAATTATGAAAGCATAAAGTTTGAGCCTGAA	1256
Db	1906	TCATCACCATTAGAAGC---TTCTTCAGTTAATTATGAAAGCATAAAACATGAGCCTGAA	1962
Qy	1257	AATCCCCCACCATATGAGGAGGCCATGAATGTATCACTAAAAAAGAATCAGGAATGAAT	1316
Db	1963	AATCCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAGTATCAGGAATAAAG	2022
Qy	1317	GAAGAAATCACAGAGCCTGAAGGTATTAGTGTAGCTGTTCAGGAAACAGAAGCTCCTTAT	1376
Db	2023	GAAGAAATTAAAGAGCCTGAAAAATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTAT	2082
Qy	1377	ATATCTATTGCATGTGATTTAATTAAAGAAACAAAGATCTCTACTGAACCGACTCCAGAT	1436
Db	2083	ATATCTATTGCATGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAACCGACTCCGAT	2142
Qy	1437	TTCTCTAGTTATTTCAGAAATAGCAGAAGTTGCACAGCCAGTGCCCGAGCATTCTGAGCTA	1496
Db	2143	TTCTCTGATTATTTCAGAAATGGCAAAAGTTGAACAGCCAGTGCCTGATCATTCTGAGCTA	2202

Qy	1497	GTTGAAGATTCTCTCCCCGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCC	1556
Db	2203	GTTGAAGATTCTCTCACCTGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCT	2262
Qy	1557	GAAGTTCCACAAAAACAAGATGAAGCTGTAATACTTGTGAAAGAAAACCTCACTGAAATT	1616
Db	2263	GACGTTCCACAAAAACAAGATGAAACTGTGATGCTTGTGAAAGAAAGTCTCACTGAGACT	2322
Qy	1617	TCATCTGAGTCAATGACAGGACATGACAATAAGGGAAAACTCAGTGCTTCACCATCACCT	1676
Db	2323	TCATTTGAGTCAATGATAGAATATGAAAATAAGGAAAAAACTCAGTGCTTTGC---CACCT	2379
Qy	1677	GAGGGAGGAAAACCGTATTTGGAGTCTTTTCAGCCCAGTTTAGGCATCACAAAAGATACC	1736
Db	2380	GAGGGAGGAAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATACC	2439
Qy	1737	TTAGCACCTGATGAAGTTTCAGCATTGACCCAAAAGGAGAAAAATCCCTTTGCAGATGGAG	1796
Db	2440	CTGTTACCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAAATTCCTTTGCAGATGGAG	2499
Qy	1797	GAGCTCAATACTGCAGTTTATTCAAGTGATGGCTTATTCATTGCTCAGGAAGCAAACCTA	1856
Db	2500	GAGCTCAGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGATA	2559
Qy	1857	AGAGAAAGTGAAACATTTTCAGATTTCATCTCCGATTGAGATTATAGATGAGTTCCCGACC	1916
Db	2560	AGAGAAACTGAAACGTTTTTCAGATTTCATCTCCAATTGAAATTATAGATGAGTTCCCTACA	2619
Qy	1917	TTTGTCAGTTCTAAAGCAGATTCTTCTCCTACATTAGCCAGGGAATACACTGACCTAGAA	1976
Db	2620	TTGATCAGTTCTAAACTGATTCATTTTCTAAATTAGCCAGGGAATATACTGACCTAGAA	2679
Qy	1977	GTAGCCACAAAAGTGAAATTGCTGACATCCAGGATGGAGCTGGGTCATTGGCTTGTGCA	2036
Db	2680	GTATCCACAAAAGTGAAATTGCTAATGCCCGGATGGAGCTGGGTCATTGCCTTGCACA	2739
Qy	2037	GGATTGCCCCATGACCTTTCTTTCAAGAGTATACAACC-----TAAAGAGGAAGTTCAT	2090
Db	2740	GAATTGCCCCATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCAGT	2799
Qy	2091	GTCCCAGATGAGTTCTCCAAAGATAGGGGTGATGTTTCAAAGGTGCCCGTACTGCCTCCA	2150
Db	2800	TTCTCAGATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCA	2859
Qy	2151	GATGTTTCTGCTTTGGATGCTCAAGCAGAGATAGGCAGCATAGAAAAACCCAAAGTTCTT	2210
Db	2860	GATGTTTCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTT	2919
Qy	2211	GTGAAAGAAGCCGAGAGAAAACCTCCTTCTGATACAGAAAAAGAGCGAAGATCTCCATCT	2270
Db	2920	GTGAAAGAAGCTGAGAAAAAACTTCCTTCCGATACAGAAAAAGAGGACAGATCACCATCT	2979
Qy	2271	GCTATATTTTCAGCAGAGCTGAGTAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGAC	2330
Db	2980	GCTATATTTTCAGCAGAGCTGAGTAAACTTCAGTTGTTGACCTCCTGTACTGGAGAGAC	3039

Qy 2331 ATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCTTGTTCCCTGCTGCTCTCGCTGACAGTA 2390
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 Db 3040 ATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCCTATTCCTGCTGCTTTTCATTGACAGTA 3099
 Qy 2391 TTCAGCATTGTGAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCTGTGACTATCAGC 2450
 |||||
 Db 3100 TTCAGCATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGC 3159
 Qy 2451 TTTAGGATATATAAGGGTGTGATCCAGGCTATCCAGAAATCTGATGAAGGCCACCCATTC 2510
 |||||
 Db 3160 TTTAGGATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTC 3219
 Qy 2511 AGGGCATATTTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGCAAT 2570
 |||||
 Db 3220 AGGGCATATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGTAAT 3279
 Qy 2571 TCTGCTCTTGGTCATGTGTAAGTGCACAATAAAAGAACTCAGACGCCTCTTCTTAGTTGAT 2630
 |||||
 Db 3280 TCTGCTCTTGGTCATGTGAAGTGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGAT 3339
 Qy 2631 GATTTAGTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCC 2690
 |||||
 Db 3340 GATTTAGTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCC 3399
 Qy 2691 TTGTTCAATGGTCTGACACTACTAATTTTGGCTCTGATTTCACTCTTCAGTGTTCCCTGTT 2750
 |||||
 Db 3400 TTGTTTAATGGTCTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTTCCCTGTT 3459
 Qy 2751 ATTTATGAACGGCATCAGGCGCAAATAGATCATTATCTGGGACTTGCAAATAAGAATGTT 2810
 |||||
 Db 3460 ATTTATGAACGGCATCAGGCGCAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTT 3519
 Qy 2811 AAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGAATGA 2870
 |||||
 Db 3520 AAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGAATGA 3579

RESULT 10

US-09-893-348-17

; Sequence 17, Application US/09893348

; Patent No. US20020072493A1

; GENERAL INFORMATION:

; APPLICANT: EISENBACH-SCHWARTZ, Michal

; APPLICANT: COHEN, Irun R.

; APPLICANT: BESERMAN, Pierre

; APPLICANT: MOSONEGO, Alon

; APPLICANT: MOALEM, Gila

; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USES

; FILE REFERENCE: EIS-SCHWARTZ=2A

; CURRENT APPLICATION NUMBER: US/09/893,348

; CURRENT FILING DATE: 2001-06-28

; PRIOR APPLICATION NUMBER: US 09/314,161

; PRIOR FILING DATE: 1999-05-19

; PRIOR APPLICATION NUMBER: US 09/218,277

; PRIOR FILING DATE: 1998-12-22

; PRIOR APPLICATION NUMBER: PCT/US98/14715

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; PRIOR FILING DATE: 1998-07-21
; PRIOR APPLICATION NUMBER: IL 124500
; PRIOR FILING DATE: 1998-05-19
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 4684
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (253)..(3744)
; OTHER INFORMATION:
US-09-893-348-17
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Query Match          56.9%;  Score 2179.4;  DB 9;  Length 4684;
Best Local Similarity 78.2%;  Pred. No. 0;
Matches 3008;  Conservative 0;  Mismatches 731;  Indels 110;  Gaps 28;
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Qy      1 CTATCTCCTCTCTCAGCCGCTGCTTTTAAAGAACGTGAATACCTTGGTGATTTACCAGCA 60
        ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      928 CTATCTCCTCTCTCAACTGTTTCTTTAAAGAACATGGATACCTTGGTAACTTATCAGCA 987

Qy      61 GTACTGCCCCACTGAAGGAACACTTCCAGCAACTTCAAATGAAGCTTCTAAAGCATTCTCA 120
        || | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      988 GTGTCATCCTCAGAAGGAACAATTGAAGAACTTTAAATGAAGCTTCTAAAGAGTTGCCA 1047

Qy      121 GAGAAGGCCAAAAAATCCATTTGTAGAGAGAAATTTAACAGAATTTTCAGAATTGGAATAT 180
        ||| | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1048 GAGAGGGCAACAAATCCATTTGTAAATAGAGATTTAGCAGAATTTTCAGAATTAGAATAT 1107

Qy      181 TCAGAAATGGAATCATCATTCAGTGGCTCTCAAAAGGCAGAACCTGCCGTAACAGTAGCG 240
        ||| | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1108 TCAGAAATGGGATCATCTTTTAAAGGCTCCCCAAAAGGAGAGTCAGCCATATTAGTAGAA 1167

Qy      241 AATCCTAGGGACGAAATAGTTGTGAGGAGTAGAGATAAAGAAGAGGACTTAGTTAGTCTT 300
        || | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1168 AACACTAAGGAAGAAGTAATTGTGAGGAGTAAAGACA---AAGAGGATTTAGTTTGTAGT 1224

Qy      301 AACATCCTTCATACTCAGCAGGAGTTATCTACAGTCCCTACGAAATCAGTTGAAGAAGAA 360
        ||| | | | | | | | | | | | | | | | | | | | | | | | |
Db      1225 GCAGCCCTTCACAGTCCACAAGAATCACCT-----GTGGGTAAAGAA 1266

Qy      361 GATAGAGTTCTGTCTCCAGAAAAAACAAGGACAGTTTTTAAGGAAAAGGGAGTTGCAGCA 420
        || | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1267 GACAGAGTTGTGTCTCCAGAAAAGACAATGGACATTTTAAATGAAATGCAGATGTCAGTA 1326

Qy      421 GAAGCTTCTATGGGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTG 480
        | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1327 GTAGCACCTGTGAGGGAAGAGTATGCAGACTTTAAGCCATTTGAACAAGCATGGGAAGTG 1386

Qy      481 AAAGATACTTACAAGCAAGATAGTGATGTTTTGATTGCTGGAGGTAATATAGAGAGCAAA 540
        ||| | | | | | | | | | | | | | | | | | | | | | | | |
Db      1387 AAAGATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCTAAT----- 1434

Qy      541 TTGGAAGGTAAAGTGGATAAGAAACACTTTTCAGATAGCCTTGAACAAACAAATCGTGAA 600
        ||| | | | | | | | | | | | | | | | | | | | | | | | |
```

Db	1435	GTGGAAAGTAAAGTGGACAGAAAATGCTTGGAGATAGCCTGGAGCAAAAAGTCTTGGG	1494
Qy	601	AAAGATAGTGAAAGCAGTAATGATGACACTTCATTTCCAGTACACCAGAAGCTGTAAGA	660
Db	1495	AAGGATAGTGAAAGCAGAAATGAGGATGCTTCTTTCCCCAGTACCCCAGAACCTGTGAAG	1554
Qy	661	GGTGGTTCCGGAGCGTACATCACGTGTGCTCCCTTTAACCCAACAAGTGAAGTGTTC	720
Db	1555	GACAGCTCCAGAGCATATATTACCTGTGCTTCCTTTACCTCAGCAACCGAAAGCACCACA	1614
Qy	721	ACAAACATTTTTCCCTTGTTGGAAGATCATACTTCGGAAAATAAGACAGATGAAAAAAG	780
Db	1615	GCAAACACTTTCCCTTTGTTAGAAGATCATACTTCAGAAAATAAAACAGATGAAAAAAA	1674
Qy	781	ATAGAA-AAAAAAGGCACAAATTGTAACAGAGAAGAATGCAAGTGTCAAGACATCAAAC	839
Db	1675	ATAGAAGAAAGGAAGGCCCAAATTATAACAGAGAAGA---CTAGCCCCAAAACGTCAAAT	1731
Qy	840	CCTTTCCTTATGGCAGCACAGGAGTCTAAGACAGATTACGTTACAACAGATCATGTGTCA	899
Db	1732	CCTTTCCTTGTAGCAGTACAGGATTCTGAGGCAGATTATGTTACAACAGATACCTTATCA	1791
Qy	900	AAGGTGACCGAGGAAGTAGTGGCAAACATGCCTGAAGGTCTAACCCAGATTTGGTTCAG	959
Db	1792	AAGGTGACTGAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGCCAGATTTAGTTTCAG	1851
Qy	960	GAAGCATGTGAAAGTGAATTGAATGAAGCTACTGGTACAAAAATTGCCTTTGAAACAAAA	1019
Db	1852	GAAGCATGTGAAAGTGAAGTGAATGAAGCCACAGGTACAAAGATTGCTTATGAAACAAAA	1911
Qy	1020	ATGGACCTGGTTCAAACCTCAGAAGCTGTGCAGGAGTCACTTTACCCTGTAACACAGCTT	1079
Db	1912	GTGGACTTGGTCCAAACATCAGAAGCTATACAAGAATCACTTTACCCACAGCACAGCTT	1971
Qy	1080	TGCCCATCTTTTGAAGAATCTGAAGCTACTCCGTCACCGGTTTTGCCTGACATTGTCATG	1139
Db	1972	TGCCCATCATTTGAGGAAGCTGAAGCAACTCCGTCACCAGTTTTGCCTGATATTGTTATG	2031
Qy	1140	GAAGCACCATTAAATTCTGTAGTTCCTAGTGCTGGTGCTTCTGCAGTGCAGCTCAGTTCA	1199
Db	2032	GAAGCACCATTAAATTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAGTGCAGCCAGTGTA	2091
Qy	1200	TCACCATTAGAACTCTTCCTTCAGTTAATTATGAAAGCATAAAGTTTGAGCCTGAAAT	1259
Db	2092	TCCCCACTGGAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGCTTGAGCCTGAAAC	2151
Qy	1260	CCCCCACCATATGAGGAGGCCATGAATGTATCACTAAAAAAGAATCAGGAATGAATGAA	1319
Db	2152	CCCCCACCATATGAAGAAGCCATGAATGTAGCACT---AAAAGCTTTGGGAACAAAGGAA	2208
Qy	1320	GAAATCACAGAGCCTGAAGGTATTAGTGTAGCTGTTTCAGGAAACAGAAGCTCCTTATATA	1379
Db	2209	GGAATAAAAGAGCCTGAAAGTTTAAATGCAGCTGTTTCAGGAAACAGAAGCTCCTTATATA	2268
Qy	1380	TCTATTGCATGTGATTTAATTAAAGAAACAAAGATCTCTACTGAACCGACTCCAGATTTTC	1439
Db	2269	TCCATTGCGTGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTTTC	2328

Qy		1440 TCTAGTTATTTCAGAAATAGCAGAAGTGTGCACAGCCAGTGCCCAGCATTCCTGAGCTAGTT	1499
Db		2329 TCTAATTATTTCAGAAATAGCAAAAATTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAGTG	2388
Qy		1500 GAAGATTTCCTCCCCGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCCGAA	1559
Db		2389 GAGGATTTCCTCACCTGAATCTGAACCAGTTGACTTATTTAGTGATGATTCGATTTCCTGAA	2448
Qy		1560 GTTCCACAAAAACAAGATGAAGCTGTAATACTTGTGAAAGAAAACCTCACTGAAATTTCA	1619
Db		2449 GTCCACAAACACAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGAAGTGTC-	2507
Qy		1620 TCTGAGTCAATGACAGGACATGACAATAAGGGGAAAACCTCAGTGCTTCACCATCACCTGAG	1679
Db		2508 -----TGAGACAGTAGCCCAGCACAAAGAGGAGAGACTTAGTGCCTCAC---CTCAGGAG	2559
Qy		1680 GGAGGAAAACCGTATTTGGAGTCTTTTCAGCCCAGTTTAGGCATCACAAAAGATACCTTA	1739
Db		2560 CTAGGAAAGCCATATTTAGAGTCTTTTCAGCCCAATTTACATAGTACAAAAGATGC---T	2616
Qy		1740 GCACCTGATGAAGTTTTAGCATTGACCCAAAAGGAGAAAATCCCTTTGCAGATGGAGGAG	1799
Db		2617 GCATCTAATGACATTCCAACATTGACCAAAAAGGAGAAAATTTCTTTGCAAATGGAAGAG	2676
Qy		1800 CTCAATACTGCAGTTTATTCAAGTGATGGCTTATTCATTGCTCAGGAAGCAAACCTAAGA	1859
Db		2677 TTТААТAСТGСАТТТAСТСAAATGATGACTTACTTTCTTCTAAGGAAGACAAATAAAA	2736
Qy		1860 GAAAGTGAAACATTTTCAGATTCACTCTCCGATTGAGATTATAGATGAGTTCCCGACCTTT	1919
Db		2737 GAAAGTGAAACATTTTCAGATTCACTCTCCGATTGAGATAATAGATGAATTTCCACGTTT	2796
Qy		1920 GTCAGTTCTAAAGCAGATTCTTCTCCTACATTAGCCAGGGAATACACTGACCTAGAAGTA	1979
Db		2797 GTCAGTGCTAA--AGATGATTCTCCTAAATTAGCCAAGGAGTACACTGATCTAGAAGTA	2853
Qy		1980 GCCCACAAAAGTGAAATTGCTGACATCCAGGATGGAGCTGGGTCATTGGCTTGTGCAGGA	2039
Db		2854 TCCGACAAAAGTGAAATTGCTAATATCCAAAGCGGGGCAGATTCAATTGCCTTGCTTAGAA	2913
Qy		2040 TTGCCCATGACCTTTCTTTCAAGAGTATACAACCTAAAGAGGAAGTTCATGTCCAGAT	2099
Db		2914 TTGCCCTGTGACCTTTCTTTCAAGAATATATATCCTAAAGATGAAGTACATGTTTCAGAT	2973
Qy		2100 GAGTTCTCCAAAGATAGGGGTGATGTTTCAAAGGTGCCCGTACTGCCTCCAGATGTTTCT	2159
Db		2974 GAATTCTCCGAAATAGGTCCAGTGTATCTAAGGCATCCATATCGCCTTCAAATGTCTCT	3033
Qy		2160 GCTTTGGATGCTCAAGCAGAGATAGGCAGCATAGAAAAACCCAAAGTTCTTGTGAAAGAA	2219
Db		3034 GCTTTGGAACCTCAGACAGAAATGGGCAGCATAGTTAAATCCAAATCACTTACGAAAGAA	3093
Qy		2220 GCCGAGAGAAAACCTTCCTTCTGATACAGAAAAAGAGCGAAGATCTCCATCTGCTATATTT	2279
Db		3094 GCAGAGAAAAAACTTCCTTCTGACACAGAGAAAGAGGACAGATCCCTGTGAGCTGTATTG	3153

Qy	2280	TCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAGAAG	2339
Db	3154	TCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAGAAG	3213
Qy	2340	ACTGGAGTGGTGTGTTGGTGCCAGCTTGTTCCCTGCTGCTCTCGCTGACAGTATTCAGCATT	2399
Db	3214	ACTGGAGTGGTGTGTTGGTGCCAGCTTATTCCTGCTGCTGTCTCTGACAGTGTTCAGCATT	3273
Qy	2400	GTGAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATA	2459
Db	3274	GTCAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCGGTGACTATCAGCTTTAGGATA	3333
Qy	2460	TATAAGGGTGTGATCCAGGCTATCCAGAAATCTGATGAAGGCCACCCATTTCAGGGCATAT	2519
Db	3334	TATAAGGGCGTGATCCAGGCTATCCAGAAATCAGATGAAGGCCACCCATTTCAGGGCATAT	3393
Qy	2520	TTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTTCAGAAGTACAGCAATTCTGCTCTT	2579
Db	3394	TTAGAATCTGAAGTTGCTATATCAGAGGAATTGGTTTCAGAAATACAGTAATTCTGCTCTT	3453
Qy	2580	GGTCATGTAACTGCACAATAAAAGAACTCAGACGCCTCTTCTTAGTTGATGATTTAGTT	2639
Db	3454	GGTCATGTGAACAGCACAATAAAAGAACTGAGGCGGCTTTTCTTAGTTGATGATTTAGTT	3513
Qy	2640	GATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTCAAT	2699
Db	3514	GATTCCCTGAAGTTTGCAGTGTTGATGTGGGTGTTTACTTATGTTGGTGCCTTGTTCAAT	3573
Qy	2700	GGTCTGACACTACTAATTTTGGCTCTGATTTCACTCTTCAGTGTTCTGTTATTTATGAA	2759
Db	3574	GGTCTGACACTACTGATTTTAGCTCTGATCTCACTCTTCAGTATTCTGTTATTTATGAA	3633
Qy	2760	CGGCATCAGGCGCAAATAGATCATTATCTGGGACTTGCAAATAAGAATGTTAAAGATGCT	2819
Db	3634	CGGCATCAGGTGCAGATAGATCATTATCTAGGACTTGCAAACAAGAGTGTTAAGGATGCC	3693
Qy	2820	ATGGCTAAAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGAATGAGAAAGCCTG	2879
Db	3694	ATGGCCAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCAGATTGAAAAGCCCC	3753
Qy	2880	AAAGAGTTAACAATAGAGGAGTTTATCTTTAAAGGGGATATTCATTTGATTCCATTGGGG	2939
Db	3754	AA-----ACAGAAGTTCATCTTTAAAGGGGACACTCACTTGATTAC----GGG	3797
Qy	2940	AGGGTCAGGGAAGAACAAAGCCTTGACATTGCAGTGCAGTTTCACAGATCTTTATTTT	2999
Db	3798	GGTGGGAGGGTCAGGGGTGAGCCCTTGGTGGCCGTGCGGTTT--CAGCTCTTTATTTT	3855
Qy	3000	GCAACGCAGTGTCTGAGGAAAAATGACCTGTCTTGACTGCCCTGTGTTTCATCATCTTAAG	3059
Db	3856	GCAGTGCAGTGTGTTGAGGAAAAATTACCTGTCTTGACTT-CCTGTGTTTATCATCTTAAG	3914
Qy	3060	TATTGTAAGCTGCTATGTATGGATTTAAATCGTAATCATATTTGTTTTCTGTATGAGG	3119
Db	3915	TATTGTAAGCTGCTGTGTATGGATCT-CATTGTAGTCACACTTGTCTTCCCAATGAGGC	3973
Qy	3120	CACTGGTGAATAAACAAAGATCTGAGAAAGCTGTATATTACACTTTGTGCGAGGTAGTCT	3179

Query Match		48.7%;	Score 1866;	DB 12;	Length 3492;
Best Local Similarity		80.9%;	Pred. No. 0;		
Matches 2325;		Conservative	0;	Mismatches 500;	Indels 49; Gaps 11;

Qy	1	CTATCTCCTCTCTCAGCCGCTGCTTTTAAAGAACGTGAATACCTTGGTGATTACCAGCA	60
Db	664	CTATCTCCTCTCTCAACTGTTTTCTTTTAAAGAACACGGATACTTGTAACCTTATCAGCA	723
Qy	61	GTA CTG C C C A C T G A A G G A A C A C T T C C A G C A A C T T C A A A T G A A G C T T C T A A A G C A T T C T C A	120
Db	724	GTGGCATCCACAGAAGGAAC TATTGAAGAACTTTAAATGAAGCTTCTAGAGAATTGCCA	783
Qy	121	GAGAAGGCCAAAAATCCATTTGTAGAGAGAAATTTAACAGAATTTTCAGAATTGGAATAT	180
Db	784	GAGAGGGCAACAAATCCATTTGTAAATAGAGAGTCAGCAGAGTTTTTCAGTATTAGAATAC	843
Qy	181	TCAGAAATGGAATCATCATT CAGTGGCTCTCAA AAGGCAGAACCTGCCGTAACAGTAGCG	240
Db	844	TCAGAAATGGGATCATCTTTCAATGGCTCCCCAAAAGGAGAGTCAGCCATGTTAGTAGAA	903
Qy	241	AATCCTAGGGACGAAATAGTTGTGAGGAGTAGAGATAAAGAAGAGGACTTAGTTAGTCTT	300
Db	904	AACACTAAGGAAGAAGTAATTGTGAGGAGTAAAGACA---AAGAGGATTTAGTTTGTAGT	960
Qy	301	AACATCCTTCATACTCAGCAGGAGTTATCTACAGTCCTTACGAAATCAGTTGAAGAAGAA	360
Db	961	GCAGCCCCTTCATAATCCACAAGAGTCACCTGCGACCCTTACTAAAGTGGTTAAAGAAGAC	1020
Qy	361	GATAGAGTTCTGTCTCCAGAAAAACAAAGGACAGTTTTTAAGGAAAAGGGAGTTGCAGCA	420
Db	1021	G---GAGTTATGTCTCCAGAAAAGACAATGGACATTTTAAATGAAATGAAAATGTCAGTG	1077
Qy	421	GAAGCTTCTATGGGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTG	480
Db	1078	GTAGCACCTGTGAGGGAAGAGTATGCAGATTTTAAAGCCATTTGAACAAGCATGGGAAGTG	1137
Qy	481	AAAGATACTTACAAGCAAGATAGTGATGTTTTGATTGCTGGAGGTAATATAGAGAGCAAA	540
Db	1138	AAAGATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCTAATA-----	1186
Qy	541	TTGGAAGGTAAAGTGGATAAGAAACACTTTTCAGATAGCCTTGAACAAACAATCGTGAA	600
Db	1187	-TGGAAAGTAAAGTGGACAAAAAATGCTTTGAAGATAGCCTGGAGCAAAAAAGTCATGGG	1245

Qy	601	AAAGATAGTGAAAGCAGTAATGATGACACTTCATTTCCCCAGTACACCAGAAGCTGTAAGA	660
Db	1246	AAGGATAGTGAAAGCAGAAATGAGAATGCTTCTTTCCCCAGTACCCCAGAACTTGTGAAG	1305
Qy	661	GGTGGTTCCGGAGCGTACATCACGTGTGCTCCCTTTAACCCAACAACGAGAATGTTTCA	720
Db	1306	GACGGCTCCAGAGCGTACATCACCTGTGATTCCCTTTACCTCAGCAACCGAGAGTACTGCA	1365
Qy	721	ACAAACATTTTTCCCTTGTTGGAAGATCATACTTCGGAATAAGACAGATGAAAAAAG	780
Db	1366	GCAAACATTTTTCCCTGTGCTAGAAGATCACACTTCAGAAAAATAAACAGATGAAAAAAA	1425
Qy	781	ATAGAA-AAAAAAGGCACAAATTGTAACAGAGAAGAATGCAAGTGTCAAGACATCAAAC	839
Db	1426	ATAGAAGAAAGGAAGGCCAAATTATAACAGAGAAGA---CTAGCCCCAAAACGTCAAAT	1482
Qy	840	CCTTTCCTTATGGCAGCACAGGAGTCTAAGACAGATTACGTTACAACAGATCATGTGTCA	899
Db	1483	CCTTTCCTTGTAGCAATACATGATTCCGAGGCAGATTATGTCACAACAGATAATTTATCA	1542
Qy	900	AAGGTGACCGAGGAAGTAGTGGCAAACATGCCTGAAGGTCTAACCCCAGATTTGGTTCAG	959
Db	1543	AAGGTGACTGAGGCAGTAGTGGCAACCATGCCTGAAGGTCTAACGCCAGATTTAGTTCAG	1602
Qy	960	GAAGCATGTGAAAGTGAATTGAATGAAGCTACTGGTACAAAAATTGCCTTTGAAACAAAA	1019
Db	1603	GAAGCATGTGAAAGTGAAGTGAACGAAGCCACAGGTACAAAGATTGCTTATGAAACAAAA	1662
Qy	1020	ATGGACCTGGTTCAAACCTCAGAAGCTGTGCAGGAGTCACTTTACCCTGTAACACAGCTT	1079
Db	1663	GTGGACTTGGTCCAGACATCAGAAGCTATACAAGAGTCAATTTACCCACAGCACAGCTT	1722
Qy	1080	TGCCCATCTTTTGAAGAATCTGAAGCTACTCCGTCACCGGTTTTGCCTGACATTGTCATG	1139
Db	1723	TGCCCATCATTGTAGGAAGCTGAAGCAACTCCGTCACCAGTTTTGCCTGATATTGTTATG	1782
Qy	1140	GAAGCACCATTAAATTCTGTAGTTCCTAGTGCTGGTGCTTCTGCAGTGCAGCTCAGTTCA	1199
Db	1783	GAAGCTCCATTAAATTCTCTCCTTCCAAGCACTGGTGCTTCTGTAGCGCAGCCAGTGCA	1842
Qy	1200	TCACCATTAGAACTCTTCCTTCAGTTAATTATGAAAGCATAAAGTTTGAGCCTGAAAAT	1259
Db	1843	TCCCCACTAGAAGTACCGTCTCCAGTTAGTTATGACGGTATAAAGCTTGAGCCTGAAAAT	1902
Qy	1260	CCCCCACCATATGAGGAGGCCATGAATGTATCACTAAAAAAGAATCAGGAATGAATGAA	1319
Db	1903	CCCCCACCATATGAAGAAGCCATGAGTGTAGCACTAAAAA---CATCGGACGCAAAGGAA	1959
Qy	1320	GAAATCACAGAGCCTGAAGGTATTAGTGTAGCTGTTTCAAGAAACAGAAGCTCCTTATATA	1379
Db	1960	GAAATTAAAGAGCCTGAAAGTTTTAATGCAGCTGCTCAGGAAGCAGAAGCTCCTTATATA	2019
Qy	1380	TCTATTGCATGTGATTTAATTAAAGAAACAAAGATCTCTACTGAACCGACTCCAGATTTT	1439
Db	2020	TCCATTGCATGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGGGTTC	2079

Qy	1440	TCTAGTTATTTCAGAAATAGCAGAAGTTGCACAGCCAGTGCCCGAGCATTCTGAGCTAGTT	1499
Db	2080	TCTAATTATTTCAGAAATAGCAAATTTGAGAAGTCGGTACCTGATCACTGTGAGCTCGTG	2139
Qy	1500	GAAGATTCCCTCCCCCGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCCGAA	1559
Db	2140	GATGATTCCCTCACCCGAATCTGAACCAGTTGACTTATTTAGTGATGATTGATTTCCTGAA	2199
Qy	1560	GTTCCACAAAAACAAGATGAAGCTGTAATACTTGTGAAAGAAAACCTCACTGAAATTTCA	1619
Db	2200	GTCCACAAACACAAGAGGAGGCTGTGATGCTAATGAAGGAGAGTCTCACTGAAGT---G	2256
Qy	1620	TCTGAGTCAATGACAGGACATGACAATAAGGGAAAACCTCAGTGCTTCACCATCACCTGAG	1679
Db	2257	TCTGAGACAGTAACACAACACAACATAAGGAGAGACTTAGTGCTTCAC---CTCAGGAG	2313
Qy	1680	GGAGGAAAACCGTATTTTGGAGTCTTTTCAGCCCAAGTTTAGGCATCACAAAAGATACCTTA	1739
Db	2314	GTAGGAAAGCCATATTTAGAGTCTTTTCAGCCCAATTTACATATTACAAAAGATGC---T	2370
Qy	1740	GCACCTGATGAAGTTTCAGCATTGACCCAAAAGGAGAAAATCCCTTTGCAGATGGAGGAG	1799
Db	2371	GCATCTAATGAAATTCACACATTGACCAAAAAGGAGACAATTTCTTTGCAAATGGAAGAG	2430
Qy	1800	CTCAATACTGCAGTTTATTCAAGTGATGGCTTATTCATTGCTCAGGAAGCAAACCTAAGA	1859
Db	2431	TTTAATACTGCAATTTATTCCAATGATGACTTACTTTCTTCTAAGGAAGACAAAATGAAA	2490
Qy	1860	GAAAGTGAAACATTTTCAGATTTCATCTCCGATTGAGATTATAGATGAGTTCCCGACCTTT	1919
Db	2491	GAAAGTGAAACATTTTCAGATTTCATCTCCGATTGAGATTATAGATGAGTTTCCACATTT	2550
Qy	1920	GTCAGTTCTAAAGCAGATTCTTCTCCTACATTAGCCAGGGAATACACTGACCTAGAAGTA	1979
Db	2551	GTCAGTGCTAAAGATGATTCTCCT-----AAGGAGTACACTGACCTAGAAGTA	2598
Qy	1980	GCCCACAAAAGTGAAATTGCTGACATCCAGGATGGAGCTGGGTCATTGGCTTGTGCAGGA	2039
Db	2599	TCCAACAAAAGTGAAATTGCTAATGTCCAGAGCGGGGCCAATTCGTTGCCTTGCTCAGAA	2658
Qy	2040	TTGCCCATGACCTTTCTTTCAAGAGTATACAACCTAAAGAGGAAGTTTCATGTCCAGAT	2099
Db	2659	TTGCCCTGTGACCTTTCTTTCAAGAATACATATCCTAAAGATGAAGCACATGTCTCAGAT	2718
Qy	2100	GAGTTCTCCAAAGATAGGGGTGATGTTTCAAAGGTGCCCGTACTGCCTCCAGATGTTTCT	2159
Db	2719	GAATTCTCCAAAGTAGGTCCAGTGTATCTAAGGTGCCCTTATTGCTTCCAAATGTTTCT	2778
Qy	2160	GCTTTGGATGCTCAAGCAGAGATAGGCAGCATAGAAAAACCCAAAGTTCTTGTGAAAGAA	2219
Db	2779	GCTTTGGAATCTCAAATAGAAATGGGCAACATAGTTAAACCCAAAGTACTTACGAAAGAA	2838
Qy	2220	GCCGAGAGAAAACCTTCTTCTGATACAGAAAAAGAGCGAAGATCTCCATCTGCTATATTT	2279
Db	2839	GCAGAGGAAAACCTTCTTCTGATACAGAGAAAGAGGACAGATCCCTGACAGCTGTATTG	2898
Qy	2280	TCAGCAGAGCTGAGTAAACCTTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAGAAG	2339

Db	2899	TCAGCAGAGCTGAATAAAACTTCAGTTGTTGACCTCCTGTACTGGAGAGACATTAAGAAG	2958
Qy	2340	ACTGGAGTGGTG---TTTGGTGCCAGCTTGTTCCTGCTGCTCTCGCTGACAGTATTCAGC	2396
Db	2959	ACTGGAGTGGTGATTTTGGTGCCAGCTTATTCCTGCTGCTGTCTCTGACAGTGTTCAGC	3018
Qy	2397	ATTGTGAGTGTAAACGGCCTACATTGCCTTGGCCCTGCTCTCTGTGACTATCAGCTTTAGG	2456
Db	3019	ATTGTGAGTGTAAACGGCCTACATTGCCTTGGCCCTGCTCTCTGTGACTATCAGCTTTAGG	3078
Qy	2457	ATATATAAGGGTGTGATCCAGGCTATCCAGAAATCTGATGAAGGCCACCCATTCAGGGCA	2516
Db	3079	ATATATAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCA	3138
Qy	2517	TATTTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGCAATTCTGCT	2576
Db	3139	TATTTGGAATCTGAAGTTGCCATATCAGAGGAATTGGTTCAGAAATATAGTAATTCTGCT	3198
Qy	2577	CTTGGTCATGTAACTGCACAATAAAAGAACTCAGACGCCTCTTCTTAGTTGATGATTTA	2636
Db	3199	CTTGGTCATGTGAACAGCACAATAAAAGAAATTGAGGCGTCTCTTCTTAGTTGATGATTTA	3258
Qy	2637	GTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTT	2696
Db	3259	GTTGATTCCCTGAAGTTTGCAGTGTTGATGTGGGTATTTACTTACGTTGGTGCCTTGTTT	3318
Qy	2697	AATGGTCTGACACTACTAATTTTGGCTCTGATTTCACTCTTCAGTGTTCTGTTATTTAT	2756
Db	3319	AATGGTTTGAACACTACTGATTTTAGCTCTGATCTCACTCTTCAGTATTCCTGTTATATAT	3378
Qy	2757	GAACGGCATCAGGCGCAAATAGATCATTATCTGGGACTTGCAAATAAGAATGTTAAAGAT	2816
Db	3379	GAACGGCATCAGGCGCAGATAGATCATTATCTAGGACTTGCAAACAAGAGCGTTAAGGAT	3438
Qy	2817	GCTATGGCTAAAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGAATGA	2870
Db	3439	GCCATGGCCAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCAGAATGA	3492

RESULT 12

US-10-220-891-22

; Sequence 22, Application US/10220891

; Publication No. US20030207286A1

; GENERAL INFORMATION:

; APPLICANT: NAKAGAWARA, AKIRA

; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES HAVING CHARACTERISTICS OF ENHANCED

; TITLE OF INVENTION: EXPRESSION IN HUMAN NEUROBLASTOMA WITH FAVORABLE PROGNOSIS

; TITLE OF INVENTION: BASED ON COMPARISON BETWEEN HUMAN NEUROBLASTOMA WITH FAVORABLE

; TITLE OF INVENTION: PROGNOSIS AND HUMAN NEUROBLASTOMA WITH UNFAVORABLE PROGNOSIS

; FILE REFERENCE: 7388-73435

; CURRENT APPLICATION NUMBER: US/10/220,891

; CURRENT FILING DATE: 2003-03-07

; PRIOR APPLICATION NUMBER: JP 2000/140387

```
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: JP 2000/159195
; PRIOR FILING DATE: 2000-03-07
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 22
;   LENGTH: 1980
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-220-891-22
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Db	625	CCTAAAACTGATTCAATTTCTAAATTAGCCAGGGAATATACTGACCTAGAAGTATCCCAC	684
Qy	1986	AAAAGTGAAATTGCTGACATCCAGGATGGAGCTGGGTCAATTGGCTTGTGCAGGATTGCCC	2045
Db	685	AAAAGTGAAATTGCTAATGCCCCGGATGGAGCTGGGTCAATGCCTTGCACAGAATTGCCC	744
Qy	2046	CATGACCTTTCTTTCAAGAGTATACAACC-----TAAAGAGGAAGTTCATGTCCCAGAT	2099
Db	745	CATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCAGTTTCTCAGAT	804
Qy	2100	GAGTTCTCCAAAGATAGGGGTGATGTTTCAAAGGTGCCCCGTACTGCCTCCAGATGTTTCT	2159
Db	805	GACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCAGATGTTTCT	864
Qy	2160	GCTTTGGATGCTCAAGCAGAGATAGGCAGCATAGAAAAACCCAAAGTTCTTGTGAAAGAA	2219
Db	865	GCTTTGGCCACTCAGGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTTGTGAAAGAA	924
Qy	2220	GCCGAGAGAAAACTTCCTTCTGATACAGAAAAAGAGCGAAGATCTCCATCTGCTATATTT	2279
Db	925	GCTGAGAAAAAACTTCCTTCCGATACAGAAAAAGAGGACAGATCACCATCTGCTATATTT	984
Qy	2280	TCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAGAAG	2339
Db	985	TCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTGTACTGGAGAGACATTAAGAAG	1044
Qy	2340	ACTGGAGTGGTGTGTTGGTGCCAGCTTGTTCCTGCTGCTCTCGCTGACAGTATTCAGCATT	2399
Db	1045	ACTGGAGTGGTGTGTTGGTGCCAGCCTATTCCAGCTGCTTTCATTGACAGTATTCAGCATT	1104
Qy	2400	GTGAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATA	2459
Db	1105	GTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATA	1164
Qy	2460	TATAAGGGTGTGATCCAGGCTATCCAGAAATCTGATGAAGGCCACCCATTACAGGGCATAT	2519
Db	1165	TACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTACAGGGCATAT	1224
Qy	2520	TTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGCAATTCTGCTCTT	2579
Db	1225	CTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGTAATTCTGCTCTT	1284
Qy	2580	GGTCATGTAACTGCACAATAAAAGAACTCAGACGCCTCTTCTTAGTTGATGATTTAGTT	2639
Db	1285	GGTCATGTGAAGTGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGATGATTTAGTT	1344
Qy	2640	GATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTCAAT	2699
Db	1345	GATTCTCTGGAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAAAT	1404
Qy	2700	GGTCTGACACTACTAATTTTGGCTCTGATTTCACTCTTCAGTGTTCTGTTATTTATGAA	2759
Db	1405	GGTCTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTTCTGTTATTTATGAA	1464
Qy	2760	CGGCATCAGGCGCAAATAGATCATTATCTGGGACTTGCAAATAAGAATGTTAAAGATGCT	2819
Db	1465	CGGCATCAGGCACAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTTAAAGATGCT	1524

Query Match 26.8%; Score 1025.4; DB 15; Length 2235;
Best Local Similarity 86.7%; Pred. No. 5.2e-249;
Matches 1361; Conservative 0; Mismatches 131; Indels 77; Gaps 18;

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Qy      2304 GTTGTTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGC 2363
          |||
Db      697 GTTGTTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGC 756

Qy      2364 TTGTTCCCTGCTGCTCTCGCTGACAGTATTGAGCATTGTGAGTGTAAACGGCCTACATTGCC 2423
          | |||
Db      757 CTATTCCTGCTGCTTTTCATTGACAGTATTGAGCATTGTGAGCGTAAACAGCCTACATTGCC 816

Qy      2424 TTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAAGGGTGTGATCCAGGCTATC 2483
          |||
Db      817 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC 876

Qy      2484 CAGAAATCTGATGAAGGCCACCCATTCAGGGCATATTTGGAATCTGAAGTTGCTATATCT 2543
          |||
Db      877 CAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGAAGTTGCTATATCT 936

Qy      2544 GAGGAGTTGGTTCAGAAGTACAGCAATTCTGCTCTTGGTCATGTAACTGCACAATAAAA 2603
          |||
Db      937 GAGGAGTTGGTTCAGAAGTACAGTAATTCTGCTCTTGGTCATGTGAAGTGCACGATAAAG 996

Qy      2604 GAACTCAGACGCCTCTTCTTAGTTGATGATTAGTTGATTCTCTGAAGTTTGCAGTGTTG 2663
          |||
Db      997 GAACTCAGGCGCCTCTTCTTAGTTGATGATTAGTTGATTCTCTGAAGTTTGCAGTGTTG 1056

Qy      2664 ATGTGGGTATTTACCTATGTTGGTGCCTTGTTCAATGGTCTGACACTACTAATTTTGGCT 2723
          |||
Db      1057 ATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAAATGGTCTGACACTACTGATTTTGGCT 1116

Qy      2724 CTGATTTCACTCTTCAGTGTTCTGTTATTTATGAACGGCATCAGGCGCAAATAGATCAT 2783
          || |||
Db      1117 CTCATTTCACTCTTCAGTGTTCTGTTATTTATGAACGGCATCAGGCACAGATAGATCAT 1176

Qy      2784 TATCTGGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATC 2843
          |||
Db      1177 TATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATC 1236

Qy      2844 CCTGGATTGAAGCGTAAAGCTGAATGAGAAAGCCTGAAAGAGTTAACAATAGAGGAGTTT 2903
          |||
Db      1237 CCTGGATTGAAGCGCAAAGCTGAATGAAAACGCCCAAATAATTA-----GTAGGAGTTC 1291

Qy      2904 ATCTTTAAAGGGGATATTCAATTTGATTCCATTGGGGAGGGTCAGGGAAGAACAAGCCTT 2963
          |||
Db      1292 ATCTTTAAAGGGGATATTCAATTTGATTATACGGGGAGGGTCAGGGAAGAACGAA-CCTT 1350

Qy      2964 GACATTGCAGTGCAGTTTCAC-----AGATCTTTATTTTGTAGCAACGCAGTG-T 3011
          ||| |||
Db      1351 GACGTTGCAGTGCAGTTTCACAGATCGTTGTTAGATCTTTATTTTGTAGCCATGCAGTGT 1410

Qy      3012 CTGAGGAAAAATGACCTGTCTTGAAGTGCCTGTGTTTCATCATCTTAAGTATTGTAAGCTG 3071
          |||
Db      1411 GTGAGGAAAAATTACCTGTCTTGAAGTGCCTGTGTTTCATCATCTTAAGTATTGTAAGCTG 1470
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Qy 3072 CTATGTATGGATTTAAATCGTAATCATATTTGTTTTTCCTGTATGAGGCACTGGTGAATA 3131
 |||||
 Db 1471 CTATGTATGGATTTAAACCGTAATCATA--TCTTTTTCCTATCTGAGGCACTGGTGAAT 1528

Qy 3132 AACAAAGATCTGAGAAAGCTGTATATTACACTTTGTGCGAGGTAGTCTTGCTGTAT-TTG 3190
 || |||
 Db 1529 AAAAAAC-----CTGTATATTTTACTTTGTTGCAGATAGTCTTGCCGCATCTTG 1577

Qy 3191 GGAATTGCAAAGAAAGTGGAGCT-----GACAGAAATAACCCTTTTCACAGTTTGTGC 3244
 | | ||||| ||| ||||| | | ||| | | |||||
 Db 1578 GCAAGTTGCAGAGATGGTGGAGCTAGAAAAAAAAAAAAAAAAAGCCCTTTTCAGTTTGTGC 1637

Qy 3245 ACTGTGTACGGTCTGTGTAGGTTGATGCAGATTTTCTGAAATGAAA----TGTTTAGACG 3300
 ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1638 ACTGTGTATGGTCCGTGTAGATTGATGCAGATTTTCTGAAATGAAATGTTTGTGTTAGACG 1697

Qy 3301 AGATCATGCCACCAAGGCAGGAGTGAAAAAGCTTGCCTTTCCTGGTATGTTCTAGGTGTA 3360
 ||||| || || ||||| ||| ||||| ||| ||||| ||||| ||||| ||||| |||||
 Db 1698 AGATCATACCGGTAAAGCAGGAATGACAAAGCTTG-CTTTTCTGGTATGTTCTAGGTGTA 1756

Qy 3361 TTGTGAAATTTACTGTTGTATTAATTGCCAATATAAGTAAATATAGATTATATATATCTA 3420
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1757 TTGTGACTTTTACTGTTATATTAATTGCCAATATAAGTAAATATAGATTATA-----TA 1810

Qy 3421 TATATAGTGTTTCACGAAGCTTAGCCCTTTACCTTCCCAGCTGCCCCACAGTGCTTGATA 3480
 | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1811 TGTATAGTGTTTCACAAAGCTTAGACCTTTACCTT-CCAGCCACCCACAGTGCTTGATA 1869

Qy 3481 CT-----TCTGTCATGGGTTTTATGTGTGTAGTCCCAAAGCACATAAGCTAGGGAGAAA 3534
 | || ||||| ||||| || ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1870 TTTCAGAGTCAGTCATTGGTTATACATGTGTAGTCCCAAAGCACATAAGCTAGAAGAAGA 1929

Qy 3535 CGTACTTCTAGGCGCACTACCATCTGTTTTCAACACGAACCGACGCCATGCAAACAGAAC 3594
 || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1930 AATATTTCTAGGAGCACTACCATCTGTTTTCAACATGAA---ATGCCACACACATAGAAC 1986

Qy 3595 TCC-TCAACATAAACTTCACTGCACAGACTTACTGTAGTTAATTTTATCAC--AAACTCT 3651
 ||| ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1987 TCCAACAACATCAATTTTCATTGCACAGACTGACTGTAGTTAATTTTGTACAGAATCTAT 2046

Qy 3652 GGACTGAATCTAATGCTTCCAAAAA-----TGTTTGCAAATATCAAACATTGTTATGT 3704
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 2047 GGACTGAATCTAATGCTTCCAAAAATGTTGTTTGTGTTTGCAAATATCAAACATTGTTATGC 2106

Qy 3705 AAGAAATAT-----AAATGACGATTTATACAATTGTGGTTTAAGCTGTATTGAACT 3756
 ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 2107 AAGAAATTATTAATTACAAAATGAAGATTTATACCATTGTGGTTTAAGCTGTACTGAACT 2166

Qy 3757 AAATCTGTGGAATGCATTGTGAACTGTAAAAGCAAAGTATCAATAAAGCTTATAGACTTA 3816
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 2167 AAATCTGTGGAATGCATTGTGAACTGTAAAAGCAAAGTATCAATAAAGCTTATAGACTTA 2226

Qy 3817 AAAAAAAAA 3825
 |||||
 Db 2227 AAAAAAAAA 2235

RESULT 14

US-09-823-245A-349

; Sequence 349, Application US/09823245A

; Publication No. US20020039760A1

; GENERAL INFORMATION:

; APPLICANT: Wong, Gordon G.

; APPLICANT: Clark, Hilary

; APPLICANT: Fechtel, Kim

; APPLICANT: Agostino, Michael J.

; APPLICANT: Howes, Steven H.

; APPLICANT: Resnick, Richard J.

; APPLICANT: Gulukota, Kamalakara

; APPLICANT: Graham, James R.

; APPLICANT: Genetics Institute, Inc.

; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS

; FILE REFERENCE: GIN 6401

; CURRENT APPLICATION NUMBER: US/09/823,245A

; CURRENT FILING DATE: 2001-03-29

; PRIOR APPLICATION NUMBER: 60/194,941

; PRIOR FILING DATE: 2000-04-06

; NUMBER OF SEQ ID NOS: 631

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 349

; LENGTH: 1514

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-823-245A-349

Query Match 25.8%; Score 989.2; DB 13; Length 1514;
Best Local Similarity 85.7%; Pred. No. 6.2e-240;
Matches 1323; Conservative 0; Mismatches 143; Indels 78; Gaps 17;

QY	2335	AGAAGACTGGAGTGGTGTGTTGGTGCCAGCTTGTTTCCTGCTGCTCTCGCTGACAGTATTCA	2394
Db	1	AGAAGACTGGAGTGGTGTGTTGGTGCCAGCCTATTTCCTGCTGCTTTTCATTGACAGTATTCA	60
QY	2395	GCATTGTGAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCTGTGACTATCAGCTTTA	2454
Db	61	GCATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTA	120
QY	2455	GGATATATAAGGGTGTGATCCAGGCTATCCAGAAATCTGATGAAGGCCACCCATTCAGGG	2514
Db	121	GGATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTCAGGG	180
QY	2515	CATATTTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGCAATTCTG	2574
Db	181	CATATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGTAATTCTG	240
QY	2575	CTCTTGGTCATGTTAAGTGCACAATAAAGAACTCAGACGCCTCTTCTTAGTTGATGATT	2634
Db	241	CTCTTGGTCATGTGAAGTGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGATGATT	300
QY	2635	TAGTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCCTTGT	2694
Db	301	TAGTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCCTTGT	360
QY	2695	TCAATGGTCTGACACTACTAATTTGGCTCTGATTTCACTCTTCAGTGTTCCCTGTTATTT	2754

Db	361	TTAATGGTCTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTTCTCTGTTATTT	420
Qy	2755	ATGAACGGCATCAGGCGCAAATAGATCATTATCTGGGACTTGCAAATAAGAATGTTAAAG	2814
Db	421	ATGAACGGCATCAGGCACAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTTAAAG	480
Qy	2815	ATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGAATGAGAAA	2874
Db	481	ATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCTGAATGAAAAC	540
Qy	2875	GCCTGAAAGAGTTAACAATAGAGGAGTTTATCTTTAAAGGGGATATTCATTTGATTCCAT	2934
Db	541	GCCCAAATAATTA-----GTAGGAGTTCATCTTTAAAGGGGATATTCATTTGATTATAC	595
Qy	2935	TGGGGAGGGTCAGGGAAGAACAAGCCTTGACATTGCAGTGCAGTTTCAC-----	2984
Db	596	GGGGGAGGGTCAGGGAAGAACGAA-CCTTGACGTTGCAGTGCAGTTTCACAGATCGTTGT	654
Qy	2985	-AGATCTTTATTTTGTAGCAACGCAGTG-TCTGAGGAAAAATGACCTGTCTTGACTGCCCT	3042
Db	655	TAGATCTTTATTTTGTAGCCATGCACTGTTGTGAGGAAAAATTACCTGTCTTGACTGCCAT	714
Qy	3043	GTGTTTCATCATCTTAAGTATTGTAAGCTGCTATGTATGGATTAAATCGTAATCATATTT	3102
Db	715	GTGTTTCATCATCTTAAGTATTGTAAGCTGCTATGTATGGATTAAACCGTAATCATATCT	774
Qy	3103	GTTT--TTCCTGTATGAGGCACTGGTGAATAAACAAAGATCTGAGAAAGCTGTATATTAC	3160
Db	775	TTTTCTATCTATCTGAGGCACTGGTGGA-----ATAAAAAACCTGTATATTTT	823
Qy	3161	ACTTTGTTCGCAGGTAGTCTTGCTGTAT-TTGGGGAATTGCAAAGAAAGTGAGCTG----	3215
Db	824	ACTTTGTTGCAGATAGTCTTGCCGCATCTTGCCAAGTTGCAGAGATGGTGGAGCTAGAAA	883
Qy	3216	--ACAGAAATAACCCTTTTTCACAGTTTGTGCACTGTGTACGGTCTGTGTAGGTTGATGCA	3273
Db	884	AAAAAAAAAAAAAGCCCTTTTCAGTTTGTGCACTGTGTATGGTCCGTGTAGATTGATGCA	943
Qy	3274	GATTTTCTGAAATGAAA----TGTTTAGACGAGATCATGCCACCAAGGCAGGAGTGAAAA	3329
Db	944	GATTTTCTGAAATGAAATGTTTGTGTTAGACGAGATCATACCGTAAAGCAGGAATGACAA	1003
Qy	3330	AGCTTGCCTTTCTGCTGATGTTCTAGGTGATTGTGAAATTTACTGTTGTATTAATTGCC	3389
Db	1004	AGCTTG-CTTTTCTGCTGATGTTCTAGGTGATTGTGACTTTTACTGTTATATTAATTGCC	1062
Qy	3390	AATATAAGTAAATATAGATTATATATATCTATATATAGTGTTCACGAAGCTTAGCCCTT	3449
Db	1063	AATATAAGTAAATATAGATTATA-----TATGTATAGTGTTCACAAAGCTTAGACCTT	1116
Qy	3450	TACCTTCCCAGCTGCCCCACAGTGCTTGATACT-----TCTGTATGGGTTTTATGTGT	3503
Db	1117	TACCTT-CCAGCCACCCACAGTGCTTGATATTTTACAGAGTCAGTCATTGGTTATACATGT	1175
Qy	3504	GTAGTCCCAAAGCACATAAGCTAGGGAGAAACGTACTTCTAGGCGCACTACCATCTGTTT	3563

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Db      1176 GTAGTTCCAAAGCACATAAGCTAGAGAAGAAATATTTCTAGGAGCACTACCATCTGTTT 1235
Qy      3564 TCAACACGAACCGACGCCATGCAAACAGAACTCCTCAACATAAACTTCACTGCACAGACT 3623
        ||||| ||| || || || || | | ||||| || ||| |||||
Db      1236 TCAACATGAAATGCC-----ACACACATAGAACTCCAACATCAATTTTCATTGCACAGACT 1290
Qy      3624 TACTGTAGTTAATTTTATCAC--AAACTCTGGACTGAATCTAATGCTTCCAAAAA----- 3676
        ||||| ||||| ||||| ||| || || ||||| ||||| |||||
Db      1291 GACTGTAGTTAATTTTGTCTACAGAATCTATGGACTGAATCTAATGCTTCCAAAAATGTTG 1350
Qy      3677 --TGTTTGCAAATATCAAACATTGTTATGTAAGAAAATAT-----AAATGACGATTT 3726
        ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1351 TTTGTTTGCAAATATCAAACATTGTTATGCAAGAAATTATTAATTATAAAATGAAGATTT 1410
Qy      3727 ATACAATTGTGGTTTAAAGCTGTATTGAACTAAATCTGTGGAATGCATTGTGAACTGTAAA 3786
        |||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1411 ATACCATTGTGGTTTAAAGCTGTACTGAACTAAATCTGTGGAATGCATTGTGAACTGTAAA 1470
Qy      3787 AGCAAAGTATCAATAAAGCTTATAGACTTAAAAAAAAAAAAAAAAA 3830
        ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1471 AGCAAAGTATCAATAAAGCTTATAGACGTAAAAAACTTAGAAA 1514

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RESULT 15

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US-10-466-258-10
; Sequence 10, Application US/10466258
; Publication No. US20040132096A1
; GENERAL INFORMATION:
; APPLICANT: GLAXO GROUP LIMITED
; TITLE OF INVENTION: ASSAY
; FILE REFERENCE: P80966 GCW
; CURRENT APPLICATION NUMBER: US/10/466,258
; CURRENT FILING DATE: 2003-07-15
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 1798
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (215)..(814)
US-10-466-258-10

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Query Match          25.7%; Score 986; DB 17; Length 1798;
Best Local Similarity 86.1%; Pred. No. 4.5e-239;
Matches 1360; Conservative 0; Mismatches 140; Indels 80; Gaps 21;

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Qy      2304 GTTGGTTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGC 2363
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      248 GTTGGTTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGC 307
Qy      2364 TTGTTCCCTGCTGCTCTCGCTGACAGTATTCAGCATTGTGAGTGTAACGGCCTACATTGCC 2423
        | ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      308 CTATTCCTGCTGCTTTTCATTGACAGTATTCAGCATTGTGAGCGTAACAGCCTACATTGCC 367
Qy      2424 TTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAAGGGTGTGATCCAGGCTATC 2483

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Db	368		TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC	427
QY	2484		CAGAAATCTGATGAAGGCCACCCATTCAGGGCATATTTGGAATCTGAAGTTGCTATATCT	2543
Db	428		CAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGAAGTTGCTATATCT	487
QY	2544		GAGGAGTTGGTTCAGAAGTACAGCAATTCTGCTCTTGGTCATGTTAACTGCACAATAAAA	2603
Db	488		GAGGAGTTGGTTCAGAAGTACAGTAATTCTGCTCTTGGTCATGTGAAGTGCACGATAAAG	547
QY	2604		GAAGTCTGACGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTG	2663
Db	548		GAAGTCTGACGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTG	607
QY	2664		ATGTGGGTATTTACCTATGTTGGTGCCTTGTTCATGGTCTGACACTACTAATTTTGGCT	2723
Db	608		ATGTGGGTATTTACCTATGTTGGTGCCTTGTTCATGGTCTGACACTACTGATTTTGGCT	667
QY	2724		CTGATTTCACT-CTTCAGTGTTCCTGTTATTTATGAACGGCATCAGGCGCAAATAGATCA	2782
Db	668		CTCATTTCACCTCCTTCAGTGTTCCTGTTATTTA-GAACGGCATCAGGCACAGATAGATCA	726
QY	2783		TTATCTGGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAAT	2842
Db	727		TTATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAAT	786
QY	2843		CCCTGGATTGAAGCGTAAAGCTGAATGAGAAAGCCTGAAAGAGTTAAACAATAGAGGAGTT	2902
Db	787		CCCTGGATTGAAGCGCAAAGCTGAATGAAAACGCCCAAATAATTA-----GTAGGAGTT	841
QY	2903		TATCTTTAAAGGGGATATTCATTTGATTCCATTGGGGAGGGTCAGGGAAGAACAAGCCT	2962
Db	842		CATCTTTAAAGGGGATATTCATTTGATTATACGGGGAGGGTCAGGGAAGAACGAA-CCT	900
QY	2963		TGACATTGCAGTGCAGTTTCAC-----AGATCTTTATTTTGTAGCAACGCAGTG-	3010
Db	901		TGACGTTGCAGTGCAGTTTCACAGATCGTTGTTAGATCTTTATTTTGTAGCCATGCACTGT	960
QY	3011		TCTGAGGAAAAATGACCTGTCTTGACTGCCCTGTGTTTCATCATCTTAAGTATTGTAAGCT	3070
Db	961		TGTGAGGAAAAATTACCTGTCTTGACTGCCATGTGTTTCATCATCTTAAGTATTGTAAGCT	1020
QY	3071		GCTATGTATGGATTTAAATCGTAATCATATTTGTTT--TTCCTGTATGAGGCACTGGTGA	3128
Db	1021		GCTATGTATGGATTTAAACCGTAATCATATCTTTTTCCTATCTATCTGAGGCACTGGTGG	1080
QY	3129		ATAAACAAAGATCTGAGAAAGCTGTATATTACACTTTGTGCGAGGTAGTCTTGCTGTAT-	3187
Db	1081		AATAAAAAAC-----CTGTATATTTTACTTTGTTGCAGATAGTCTTGCCGCATC	1129
QY	3188		TTGGGGAATTGCAAAGAAAGTGGAGCT-----GACAGAAATAACCCTTTTCACAGTTTG	3241
Db	1130		TTGGCAAGTTGCAGAGATGGTGGAGCTAGAAAAAAAAAAAAAAAAAGCCCTTTTCAGTTTG	1189
QY	3242		TGCACTGTGTACGGTCTGTGTAGGTTGATGCAGATTTTCTGAAATGAAA-----TGTTTTAG	3297

